

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 03:19:15 ; Search time 2034.91 Seconds
(without alignments)
15518.202 Million cell updates/sec ;

Title: US-09-623-304A-2

Perfect score: 1509

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Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 3595312

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl :
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2: gb_htg : *
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32: em_htg_other : *
33: em_htg_inv : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

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2	1436.6	95.2	1856	9	AF153817	AF153817 Homo sapi
3	1436.6	95.2	2089	9	AF153815	AF153815 Homo sapi
4	1436.6	95.2	3642	9	AF153809S6	AF153809S6
5	1436.6	95.2	4021	9	AF153816	AF153816 Homo sapi
6	1436.6	95.2	123211	9	AC005208	AC005208 Homo sapi
7	1214.4	80.5	1257	9	AF179353	AF179353 Homo sapi
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9	915.6	60.7	205947	2	AL592422	AL592422 Mus muscu
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ALIGNMENTS

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DEFINITION Sequence 42 from patent WO0146258.
ACCESSION AX179754
VERSION AX179754.1 GI:15132118
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1730)
Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Reddy, R.,
Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Yao, M.G.,
Gandhi, A.R., Yang, Y.T., and Khan, F.A.
TITLE: Transposers and ion channels
JOURNAL: Patent: WO 0146258-A 42 28-JUN-2001;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
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Best Local Similarity 98.7%; Freq. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

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RESULT 2

AF153817

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

1856 bp mRNA linear PRI 16-MAR-2001

Homo sapiens clone 3 inwardly-rectifying potassium channel Kir5.1 (KCNJ16) mRNA, complete cds.

AF153817

AF153817.1 GI:8132294

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1856)

Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R., Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and Karschin,A.

Genetic and functional linkage of Kir5.1 and Kir2.1 channel subunits

FEBS Lett. 491 (3), 305-311 (2001)

11240146

2 (bases 1 to 1856)

Derst,C.

Direct Submission

Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology, Deutschausstr. 2, Marburg 35037, Germany

Location/Qualifiers

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ACCESSION AF153815
VERSION AF153815.1 GI:8132290
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (Bases 1 to 2089)
Derst,C., Karschin,C., Wismeyer,E., Hirsch,J.R.,
Preisig,Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
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RESULT 4
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LOCUS AF153809S6 3642 bp DNA linear PRI 16-MAR-2001

DEFINITION Homo sapiens inwardly-rectifying potassium channel Kirs.1 (KCNJ16)

ACCESSION AF153814

VERSION AF153814.1 GI:81323310

KEYWORDS 6 of 6

SEGMENT human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 3642)
Diers, C., Karschin, C., Wischmeyer, E., Hirsch, J. R., Preisig, Muller, R., Rajan, S., Engel, H., Grzeschik, K., Daut, J. and Karschin, A.
Genetic and functional linkage of Kir5.1 and Kir2.1 channel subunits

AUTHORS

TITLE

JOURNAL FEBS Lett. 491 (3), 305-311 (2001)

PubMed 11240146

REFERENCE 2 (bases 1 to 3642)
Diers, C.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology, Deutschausstr. 2, Marburg 35037, Germany

FEATURES

source

1.3642
Location/Qualifiers

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ORIGIN

Query Match 95.2%; Score 1436.6; DB 9; Length 3642;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

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LOCUS Homo sapiens clone 2 inwardly-rectifying potassium channel,Kir5.1
DEFINITION (KCNJ16) mRNA, complete cds.
ACCESSION AF153816
VERSION AF153816.1 GI:8132292
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 4021)
AUTHORS Derst,C., Karschin,C., Wismeyer,E., Hirsch,J.R.,
Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
Karschin,A.
TITLE Genetic and functional linkage of Kir5.1 and Kir2.1 channel
subunits
JOURNAL FEBS Lett. 491 (3), 305-311 (2001)
PUBMED 11240146
REFERENCE 2 (bases 1 to 4021)
AUTHORS Derst,C.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-1999) Phillips University, Inst. f. Physiology,
Deutschausstr. 2, Marburg 35037, Germany
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Query Match 95.2%; Score 1436.6; DB 9; Length 4021;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;
Oy 1 ttaactactcaaaactaccctggaatccctaaagggacagcaagaatgagctataagc 60
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LOCUS Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete
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VERSION AC005208 GI:3365585
KEYWORDS HTG.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 17, clone hRPK.1064_E_11
JOURNAL Unpublished
2 (bases 1 to 123211)
AUTHORS Birren, B., Fasmann, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

Baker, J., Baldwin, J., Barna, N., Beckler, R., Benn, J., Boatin, C.,
Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E.,
Devon, K., Dewar, K., Donelan, L., Ettemad, S., Ferreira, P.,
Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B.,
Harris, K., Horton, L., Howland, J. C., Hul, L., Jacotot, L., Kann, L.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B.,
Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R.,
Strange-Thomann, N., Stillwell, J., Stojanovic, N., Stone, C.,
Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H.,
Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W. J., Zhao, J. and
Zody, M.
Direct Submission
Submitted (30-JUN-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 123211)
REFERENCE
AUTHORS Birren, B., Fasmann, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Baker, J., Baldwin, J., Barna, N., Beckler, R., Benn, J., Boatin, C.,
Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E.,
Devon, K., Dewar, K., Donelan, L., Ettemad, S., Ferreira, P.,
Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B.,
Harris, K., Horton, L., Howland, J. C., Jacotot, L., Kann, L.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K.,
Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R.,
Strange-Thomann, N., Stillwell, J., Stojanovic, N., Stone, C.,
Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A.,
Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W. J., Zhao, J. and Zody, M.
Direct Submission
Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 123211)
REFERENCE
AUTHORS Birren, B., Fasmann, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Baker, J., Baldwin, J., Barna, N., Beckler, R., Benn, J., Boutwell, C.,
Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K.,
Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B.,
Horton, L., Howland, J. C., Jacotot, L., Kann, L., Macdonald, P.,
Margulis, N., McEwan, P., McGurk, A., McKernan, K., Meldrum, J.,
Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J.,
Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R.,
Roberts, D., Roy, A., Strange-Thomann, N., Stillwell, J., Stojanovic, N.,
Stone, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A.,
Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W. J., Zhao, J. and Zody, M.
Direct Submission
Submitted (31-JUL-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 31, 1998 this sequence version replaced gi:3347827.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

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Query Match	95.2%;	Score 1436.6;	DB 9;	Length 123211;
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Db 108379 GACACCAAGCGAGAGAGGTCATTTAGTGCAAGTTGTCAGAGCT- GTGAAAA 108437
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Db 108733 CGCCAATT 108740

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RESULT 7
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DEFINITION Homo sapiens inward rectifier potassium channel Kir5.1 (KCNJ16)
ACCESSION AF179353
VERSION AF179353
KEYWORDS AF179353.1 GI:9957531
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Liu, Y., McKenna, E., Figueroa, D. J., Blevins, R., Austin, C. P.,
Bennett, P. B. and Swanson, R.
The human inward rectifier K+ channel subunit Kir5.1 maps to
chromosome 17q25 and is expressed in kidney and pancreas
Unpublished
TITLE 2 (bases 1 to 1257)
REFERENCE Direct Submission
AUTHORS Liu, Y. and McKenna, E.
Submitted (20-AUG-1999) Bioinformatics, Merck & Co., Inc.,
WP42-300, West Point, PA 19486, USA
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RESULT 8
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DEFINITION Mus musculus chromosome 11 clone RP23-408D5, *** SEQUENCING IN

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PROGRESS **, in unordered pieces.
ACCESSION AL662912
VERSION AL662912.10 GI:18477421
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVIFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Tracey, A.
AUTHORS 1 (sites)
TITLE Direct Submission
JOURNAL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18476962.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM408D5
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 193498 bases at least Q40
Consensus quality: 193567 bases at least Q30
Consensus quality: 193654 bases at least Q20
Insert size: 193741; sum-of-contrigs
Insert size: 190800; 1.9% error; agarose-fp
Insert coverage: 10.92x in Q20 bases; sum-of-contrigs quality
coverage: 11.24x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Best Local Similarity 78.7%; Pred. No. 2.9e-233;
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RESULT 9
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 DEFINITION Mus musculus chromosome 11 clone RP23-218016, *** SEQUENCING IN
 PROGRESS ***, in unordered pieces.
 ACCESSION AL592422
 VERSION AL592422.10 GI:17426517
 KEYWORDS HTGS, PHASE1; HTGS, ACTIVEFIN; HTGS, DRAFT; HTGS, FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (sites)
 AUTHORS Almeida, J.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Dec 8, 2001 this sequence version replaced gi:17148386.

COMMENT

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: BM218016
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: pBlasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 205628 bases at least Q40
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 Insert size: 205747; sum-of-contrasts
 Insert size: 189076; 6.5% error; agarose-fp
 Quality coverage: 11.16x in Q20 bases; sum-of-contrasts Quality
 coverage: 12.15x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES

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DB 164129 AAAATTCACAAATTTTCAATATTTAAATTTGGCTTTGGCAGTA 164171

RESULT 10
AB016197 1257 bp mRNA linear ROD 02-DEC-1998
LOCUS AB016197
DEFINITION Mus musculus Kcnj16 mRNA for inwardly rectifying potassium channel
KIR5.1, partial cds.
ACCESSION AB016197
VERSION AB016197.1 GI:3953532
KEYWORDS inwardly rectifying potassium channel KIR5.1.
SOURCE Mus musculus (strain:C57) 19 weeks old females brain cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Horio, Y.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1998) Yoshiyuki Horio, Faculty of Medicine, Osaka
University, Department of Pharmacology II, 2-2 Yamadaoka, Suita,
Osaka 565-0871, Japan (E-mail:horio@pharma2.med.osaka-u.ac.jp,
Tel:81-6-879-3512, Fax:81-6-879-3519)
REFERENCE 2 (sites)
AUTHORS Mouri,T., Kikake,N., Horio,Y., Copeland,N.G., Gilbert,D.J.,
Jenkins,N.A. and Kurauchi,Y.
TITLE Assignment of mouse inwardly rectifying potassium channel Kcnj16 to
the distal region of mouse chromosome 11
JOURNAL Genomics 54 (1), 181-182 (1998)
MEDLINE 99026146

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[illegible]

FEATURES	Location/Qualifiers
1	1000

/organism="Rattus norvegicus"

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           NFIIGALAKMATARKRAORTIRFSYFLIMRQKLCIMRIGDERNHVEGVRA
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           EILVFTITGDSIGSHOSRSSYVREILKMRHHDYEVKRYIKVNCLOPESVEY
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CDS        SPODECKEVPYOKALTLINRISMESOM
BASE COUNT 326 a 325 c 315 g 294 t
ORIGIN

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Query Match      57.7% Score 870.6 DB 10 Length 1260
Best Local Similarity 82.6% Pred. No. 2.6e-221
Matches 1043; Conservative 1; Mismatches 211; Indels 7; Gaps 4

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OY 106 ccgcagagacacatatacgtcgtagaagaagaagaagaagaagaagaagaagaaga 165
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DB 61 cctccagagacacatatacgtcgtagaagaagaagaagaagaagaagaagaagaaga 120
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DB 181 atatttcacacactctgtgacacaaaggcgcacatcttggatgtaattcttctatc 240
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DB 721 gtccagcacaatcatcatcgtgtcaccgccggaactatgttccatgaataatgaccatgag 780
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OY 826 agcctcgtatgaccttgaaccgcaagaagcagtagcccaagaataacttggagatlttggtg 885
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DB 781 agcctcgtatgaccttgaaccgcaagaagcagtagcccaagaataatgagatlttggtg 840
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OY 886 aattatcatcagcgtggtatcccatcctggaacatctcacaatctagaagccctcatgt 945
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DB 841 acattattattatcgtggtatcccatcctggaacatctcacaatctagaagccctcatgt 900
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OY 1066 gccaaagcattgactggaagaagcagcagctccaca---tagaaagcacacacagct 1122
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DB 1021 gccaaagcattgactggaagaagcagcagctccaca---tagaaagcacacacagct 1080
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DB 1141 gtcaagcgtgtgtgaagaacccctggaaggaagcagcagcagcagcagcagcagcagcag 1199
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DB 1200 gccctccttatacgaagcgtcctcctgactttaaacaangaatcctgtgtgaatcccaat 1256
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OY 1303 gt 1304
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DB 1257 gt 1258
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RESULT 12
AC025586/c 187774 bp DNA linear HTG 06-SEP-2000
LOCUS AC025586
DEFINITION Mus musculus clone RP23-320C8, WORKING DRAFT SEQUENCE, 7 unordered
pieces.
ACCESSION AC025586.3 GI:9972313
VERSION AC025586.3
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE 1 (bases 1 to 187774)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
McCormbie, M., R., Baker, J. P., Bahret, A., Bal, H., Dedhia, N. N., de la
Bastide, M., Huang, E. N., King, L., Kirchoff, K. A., Miller, B.,
Nascimento, L. U., O'Shaughnessy, A. L., Preston, R. R., Rodriguez, M. A.,
Shah, R. S., Shekher, M., Spiegel, L. A., Toth, K. and Vill, M. D.

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TITLE Mouse Genomic Sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 187774)
AUTHORS McCormbie, M. R.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA

```

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COMMENT On Sep 6, 2000 this sequence version replaced q1:8439867.
----- Genome Center
Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor

```

Laboratory
Center code: CSHL
Web site: <http://www.cshl.org/genseq>
Contact: mcombie@cshl.org

Project Information
Center project name: RP23-320C8
Center clone name: RP23-320C8

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 62545: contig of 62545 bp in length
* 62546 62975: gap of unknown length
* 62976 123025: contig of 60050 bp in length
* 123026 123454: gap of unknown length
* 123455 145175: contig of 21721 bp in length
* 145176 145604: gap of unknown length
* 145605 166987: contig of 21383 bp in length
* 166988 167416: gap of unknown length
* 167417 180022: contig of 12606 bp in length
* 180023 180451: gap of unknown length
* 180452 184785: contig of 4334 bp in length
* 184786 185215: gap of unknown length
* 185215 187774: contig of 2360 bp in length.

FEATURES
Source
1. 187774
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-320C8"

BASE COUNT 55776 a 37551 c 37806 g 54065 t 2576 others
ORIGIN

Query Match 57.1% Score 861.6; DB 2: Length 187774;
Best Local Similarity 78.1%; Pred. No. 7.4e-215;
Matches 1160; Conservative 2; Mismatches 282; Indels 41; Gaps 9;

QY 26 ccctaaaggagcaagaagaatgactatgaagcagcagcatcatcatatcatgagc 85
DB 21245 CCTTAAGAGCAAGAAAGATGAGCTATTAGGAAGTAGCTACAGATCGTCAATGTCG 21186
QY 86 aegcaaaaataccagagctaccgcaagacattatagctgagaagaagaagaaga 145
DB 21185 ACTCCAAATATCCAGGCTATCTCCAGAGCATGCCATCGTGAGAAAGAGCAAGAA 21126
QY 146 gacgaattactcaaaaagatgacagctgaatgctactcaagaacattttgagaat 205
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DB 21065 GGGGAGGCTACATGGTGTATTTTACCACTCTGTGATACCAAGTGGCCCATATCT 21006
QY 266 ttgtatattttcttatactatctctcggtgtgatattggctctgtcctttggc 325
DB 21005 TCGT-AAATTTTCTGTGGTTCATCTCTCCGGTGAATTTTGGCTTCATATTTTGG- 20946
QY 326 tcatagaccttaccatag-cgactatataatgattcagacatcacacctgtgtg-a 383
DB 20947 TCATAGCCTTTATATACGAGAACCTATTAACGATCCAGATATCACCCCTGTGTGGA 20888
QY 384 caagctcatcttccacagaggccttttctcccccctagagaccacacacacatag 443
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QY 444 atatggtatcgctgtgtactgaagaatgtctgtgcgcgtgctcatgtgtgactccca 503
DB 20827 ATACGTTACCGCTGTGTACCCGAGAGAGTGCTGTGGCTGACTGACAGTATCTTTGA 20768

QY 504 gtccatcttaagttgcatcataataataccttatcatcttgagagctgtgccaatggc 563
DB 20767 GTCCATCTCAGCTGCATATATAAACCTTTCATCATTTGAGAGCCTTGGCAAAAGTGGC 20708
QY 564 aactgtcgaagaagagaccacacacatctgcttcaagctacttgcacttataagtagag 623
DB 20707 AACTGCCGGAAGAGAGGCCACAGCCATFACGCTTACACTATTTTGGCCCTCATTTGTATGAG 20648
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QY 1401 gctatgtttatgagatgtcgtggtgaagtagtaagttaaactgtgtaaagaataatct 1460
DB 19900 TCTGTGATTTGGGA-CAGGAATGAAAGAGCAGGTAAACTTGTGTAATTAATTAATCT 19842
QY 1461 aaaaattccatagttctcagttataaactttctgttgcgga 1505
DB 19841 AAAAAATCCCAATTTTACAATTTTAAATTTTGGCTTGTGGCAGTA 19797

RESULT 13
RNTRPC9
LOCUS RNTRPC9 1155 bp mRNA linear ROD 11-JAN-1996

DEFINITION	R.rattus mRNA for inward rectifier 9.
ACCESSION	X83581
VERSION	X83581.1 GI:609671
KEYWORDS	Inward rectifier potassium channel.
SOURCE	black rat.
ORGANISM	Rattus rattus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 1155) Bond,C.T., Pessia,M., Xia,X.M., Lagrutta,A., Kavanaugh,M.P. and Adelman,J.P.
TITLE	Cloning and expression of a family of inward rectifier potassium channels
JOURNAL	Recept. Channels 2 (3), 183-191 (1994)
MEDLINE	95179470
REMARK	Erratum: [[published erratum appears in Receptors Channels 1994;2(4):following 350]]
REFERENCE	2 (bases 1 to 1155)
AUTHORS	Adelman,J.P.
TITLE	Direct Submission
JOURNAL	Submitted (19-DEC-1994) J.P. Adelman, Vollum Institute for Advanced

FEATURES	Location/Qualifiers
source	1. .1155

CDS

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Query Match	55.2%	Score 832.8	DB 10	Length 1155
Best Local Similarity	83.2%	Pred. No. 3.1e-211		
Matches	959	Conservative	1	Mismatches 181; Indels 4; Gaps 1
QY	46	atgagctatlaagagacagcatcatatlaatcatlqcgagcaaataccaggtac	105	
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QY	106	ccgccaagagacattatagctlgaagaagaagacgaagaagacgaattactlccaaaagt	165	
Db	61	CCTCCAGAGCAATGCCATAGCCGACGAAGAAGAAAGCAGAGGCGCCTGTCCCAAAAGAT	120	
QY	166	ggcagctgtaatgcttacttcaagacacatlittgagaatlgggaagctatgltgttgc	225	
Db	121	GGCACCTGTAACTGTTACTTTAAACACATTTTGGAGATGGGGGAGCTACATGTTGAT	180	
QY	226	attcttaccactctctgttgacacccaagfyggcgcatatglttgatatttcttacct	285	
Db	181	ATATTACACACACTCTGTGGATACCAAGTGGCCCATATGTGTGTATTTCTTGTGCT	240	
QY	286	tatatctctcgttgltgatatattlgtgcctgtgccttttggcttaagcccttcatatg	345	
Db	241	TACATTCTCTCGTGTGATTTATTCGGCTCCATATTTTGGCTCATATGCCCTTATATCGGA	300	

Oy	346	gacattaaatgacagacagacacacacttgctgtgacgaagccatctctcaagg	405
Dp	301	GACCTATTAAAGCGATCCAGACATCACCCCGTCGTGGACACAGTCATTCTTAAGGCT	360
Oy	406	gocctttgtcttcacctagagagaccacaacacatagatatgltatgcgtgttact	465
Dp	361	GGCTTTTATTTCTCCCTTGAGACCACCAACACACATCGGGTAGGTGTACCGTTGTGTACG	420
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Dp	481	AACACCTTCATCATTTGGGGAGCCCTTGGCAAAAGATGGCGACCCGCCGGAAGCGACCCAG	540
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Oy	706	ctccgctatacagaagacagtgaaaggaagatgacatggtcaattaaagacctcaata	765
Dp	661	CTGCCCTATTTCAGAAAGACAGCGAAGGGGGAGAGACGATGGCGCTTTAAAGACCTCAAAAC	720
Oy	766	gtcaacgagccaaatcatctctgttcccccgcgtaactatgttccatgaaattgaccatgag	825
Dp	721	GTCATATGACCGATATATCTCTGTAAACGCCAGTAGACCATTTGTCATGTAAATTACACACGAG	780
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Oy	946	ccccgaaatattctcttgtagccataggtgttlaatgtagtcttggaagtttaagagaagat	1005
Dp	901	CCCAAGAAATATCTCTGGGGACACACAGGTTTCAATGATTTGGAATGTAAGAAGAAAGTAC	960
Oy	1006	tacaaagtgaactgctctacagtttgaagaagaagtgtggaagtatatgccccctttgcagt	1065
Dp	961	TACAAGGTAAACTGCTTCCAGTTTATGAGGAAACCGTGGAAGTCTACGCCCCCTTTGTGCACT	1020
Oy	1066	gccaaagcaattgagacttgtaagaagaccagagctccaca----tagaanaaagacccacccagt	1121
Dp	1021	GCCAAACCACTGTGACTGTGAAGAGCCCAACACGCTCAACAACTTGGAGAAAAAGTCCCTGTGG	1080
Oy	1122	tcgaaagatcttgacagctgcggaacccaagcgcgaagcgaagcgaagtcattttagtgcagttgcaat	1181
Dp	1081	CCGAGAGTCTCTGACACTCTGGACACCAACACCGAGGAGATCTCTACGGCGCAGTTGCCAT	1140
Oy	1182	tgtagcagagctg 1193	
Dp	1141	GGTGAAGCAGCTG 1152	

RESULT	14			
LOCUS	AF021138			
DEFINITION	AF021138	1284 bp	mRNA	linear
	Oryctolagus cuniculus inward rectifier potassium channel (IRK1)			
	mRNA, complete cds.			
ACCESSION	AF021138			
VERSION	AF021138.1	GI:2460305		
KEYWORDS				
SOURCE	rabbit.			
ORGANISM	Oryctolagus cuniculus			
	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
	Mammalia; Eutharia; Lagomorpha; Leporidae; Oryctolagus.			

REFERENCE	1 (bases 1 to 1284)
AUTHORS	Rae,J.L. and Shepard,A.R.
TITLE	Irreversibly rectifying potassium channels in lens epithelium are from the IRK1 (Kir 2.1) family
JOURNAL	Exp. Eye Res. 66 (3), 347-359 (1998)
MEDLINE	98288410
PUBMED	9533862
REFERENCE	2 (bases 1 to 1284)
AUTHORS	Rae,J.L. and Shepard,A.R.
TITLE	Direct Submission
JOURNAL	Submitted (28-AUG-1997) Physiology and Biophysics, Mayo Foundation, 200 1st Street SW, Rochester, MN 55905, USA
FEATURES	Location/Qualifiers
SOURCE	1..1284

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gene
1. .1284
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/gene="IRK1"
/note="PCR primer designed from Mus musculus inward
rectifier k(+) channel IRK1 mRNA: GenBank Accession Number
X73052"
1. .1284

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/gene="IRK1"
/codon_start=1
/product="inward rectifier potassium channel"
/protein_id="AAB88796.1"
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/translacion="MGSVIRNRYSIVSEEDGMKLTMAVANGFGSKVYHTPOOCR
SRFPKDGHCNVQFIVNGEKQRYLADIFTCVDIRRMMLVLCFLFVLSMFEFGC
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VVRPSIYGCITDAITIGAVAKMAKPKRKNETLVFSHNAVYAMDGKICLMMRGNLR
KSHLEVAAHRAQLKLSRTISEGEYIPDQDIDNVGFSGIDRIEIVSPTIVHIDED
SPPLDLSKODMNDNDEFIVLILEGMVATANTTOCRSSVLAELIIMGHRIYVFEEDS
HYIVVDKSRFHRTYEVTNPLCSARDLAEKYYITLNNNSFCYENEVAATRSPEEDSEN
GVPSSTNDPPDILDINQASVPLEPRLRRESLI"

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Best Local Similarity	60.7%;	Pred. No. 1.3e-73;		
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Db	130	AGGACCCCTTCGTCAAAAGATAGCCACATGCCACATGCCATTCACCTATCATCACTGGGTGAG	189	
OY	202	gaatgggaagcatatgttggttgacatcttcaccactctgtgtgacaccaagtgagagcat	281	
Db	190	AAGGACACAAGATACCTTCGCACAGACTTCTTTACACAGTGTGTGACATTTCGCTGGGGATGG	249	
OY	262	atgttttgataatttcttctatctatctctctcgtgtgtgataatttggctcgtctctt	321	
Db	250	ATGCGGTTATCTTCCTGGCTGGCGCTTTGTCCTCCTGCTATTTTTTGGCTGTGTGTTT	309	
OY	322	tgagccatagcccttcatcatcattgagcgatctatataaigtaccagacatcacactgtgtt	381	
Db	310	TGCTGTATAGCTCTCTCCATGCGGATCTGTGATGCTTTAGAGAGACGAACCCCTGTGTG	369	
OY	382	gacaaagtcacattcttcaagaaggccttltgtctctccctagagaaccaaacacata	441	
Db	370	TCTGTAGGTAACACAGCTTCACAGCCCTCTCTCTTCCTCATCATGAAACCCAGACAACCATTA	429	
OY	442	gataatgttatacgtctgttatacgaagaatgttcttgagccgtgcataatgttatcttc	501	
Db	430	GGCTATGGCTTCCGGTGCTGTACACAGCAATGCCAGTTGCTGTTTATAGTGGGTTC	489	
OY	502	cagtcacattcaagtgtgcatcataaataaccttatacatgtgaagtcgtcttgagccaaatg	561	

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Oy	907	tccacttggaaacatccaccaatctagaagctcctatgttcccccagataatctcttgggc	966
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Db	970	CACCCCTATGAGCCCTGTACTCTTTGGAAGAGAGAACTATTACAAATGGACCTATTCGAGG	1029
Oy	1027	tttgaaggaagtgtygaagta	1047
Db	1030	TTCCACAAACCTATGAAAGTA	1050

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DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

RABPC Rabbit mRNA for potassium channel, complete cds.
D21057
D21057.1 GI:464193
K+ channel: potassium channel.
Oryctolagus cuniculus (strain New Zealand White) heart cDNA to
mRNA, clone RBH1K1.
Oryctolagus cuniculus.
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 2342)
Ishii,K.
Direct Submission
Submitted (02-OCT-1993) Kuniaki Ishii, Tohoku University School of
Medicine, Department of Pharmacology; 2-1 Seiry-machi Aoba-ku,
Sendai, Miyagi 980, Japan (Tel:022-274-1111(ex.2173),
Fax:022-273-6996)
2 (bases 1 to 2342)
Ishii,K., Yamagishi,T. and Taira,N.
Cloning and functional expression of a cardiac inward rectifier K+
channel
FEBS Lett. 338 (1), 107-111 (1994)
94139886
Submitted (02-Oct-1993) to DDBJ by:
Kuniaki Ishii
Department of pharmacology
Tohoku University School of Medicine
2-1 Seiry-machi, Aoba-ku
Sendai, Miyagi 980
Japan
Phone: 022-274-1111 x2173
Fax: 022-273-6996.

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THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: October 5, 2002, 03:23:25 ; Search time 211.12 seconds
(without alignments)
12271.807 Million cell updates/sec

Title: US-09-623-304A-2

Perfect score: 1509

Sequence: 1 ttactactacaaactcacc.....ttttctgttcgcgaattc 1509

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507.2	99.9	1509	AAZ21041	Human KIR5.1 Invar
2	1436.6	95.2	1730	AAD09566	Human transporter
3	1436.6	95.2	1921	AAK05088	Human brain expres
4	1436.6	95.2	1921	AAI36580	Probe #5266 used t
5	1259.4	83.5	1395	AAS92631	DNA encoding novel
6	1214.4	80.5	1257	AAF85049	Nucleotide sequenc
7	1069.6	70.9	1118	AAK17807	Human brain expres
8	1069.6	70.9	1118	AAI49699	Probe #18385 used
9	869.6	57.6	1257	AAF85050	Nucleotide sequenc

10	808	53.5	907	20	AAK35739	CDNA encoding a pr
11	763	50.6	765	20	AAK35738	CDNA encoding a pr
12	430	28.5	856	22	AAS31087	Human diagnostic a
13	314.2	20.8	1284	22	AAH21453	Human IRK1 DNA. H
14	304.4	20.2	1310	22	ABA35969	Probe #14435 for g
15	304.4	20.2	1310	22	AAK17341	Human brain expres
16	304.4	20.2	1310	22	AAI49214	Probe #17900 used
17	304.4	20.2	1310	22	ABA26076	Probe #4542 for ge
18	304.4	20.2	1310	22	AAK04606	Human brain expres
19	304.4	20.2	1310	22	AAI36079	Probe #4765 used t
20	280.4	18.6	2311	16	AAQ82904	Mouse Inward recti
21	206.6	13.7	1809	22	AAD09565	Human transporter
22	182	12.1	1260	16	AAQ97305	Human heart ATP-se
23	182	12.1	1260	19	AAV40684	Human heart ATP-se
24	181.8	12.0	1245	16	AAQ97306	Pancreatic beta ce
25	181.8	12.0	1245	16	AAV40687	Human pancreatic b
26	176.4	11.7	1095	19	AAV40691	Rat pancreatic bet
27	176.4	11.7	1095	16	AAQ97308	Rat pancreatic bet
28	176.4	11.7	1425	19	AAV40686	Rat pancreatic bet
29	172	11.4	1260	16	AAQ97307	Rat heart ATP-sens
30	172	11.4	1260	19	AAV40685	Rat heart ATP-sens
31	167.2	11.1	1827	16	AAQ82905	Rat G protein coup
32	165.6	11.0	2070	19	AAV40692	KIR3.1/KGA coding
33	165.6	11.0	2076	16	AAQ97305	Potassium KGA chan
34	162.8	10.8	7690	24	ABL33122	Human immune syste
35	162.6	10.8	7690	24	ABL33123	Human immune syste
36	155.6	10.3	2896	18	AAH84537	Human kidney invar
37	151.2	10.0	1275	18	AAH69797	Human ATP-sensitiv
38	151.2	10.0	1749	23	AAH69797	DNA encoding novel
39	151.2	10.0	1968	23	AAH69797	DNA encoding novel
40	151.2	10.0	2033	23	AAH69795	DNA encoding novel
41	148.2	9.8	1107	19	AAV53714	Human ATP-sensitiv
42	148.2	9.8	1137	19	AAV53713	Human ATP-sensitiv
43	148.2	9.8	1278	18	AAH67088	Human K-ATP channe
44	148.2	9.8	1278	19	AAV53712	Human ATP-sensitiv
45	146.6	9.7	1173	18	AAH61866	Human ATP sensitiv

ALIGNMENTS

RESULT 1	AAZ21041	standard; cDNA; 1509 BP.
ID	AAZ21041	
AC	AAZ21041	
XX		
DT	01-DEC-1999	(first entry)
XX		
DE	Human KIR5.1 Inward rectifier potassium channel alpha subunit cDNA.	
XX		
KW	Potassium channel; Inward rectifier; hypertension; renal failure;	
KW	diabetes; cystic fibrosis; hypothyroidism; hyperthyroidism; ds.	
OS	Homo sapiens.	
XX		
XX		
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PN	W09945358-A2.	
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PD	10-SEP-1999.	
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PF	02-MAR-1999;	99WO-US04549.
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PR	03-MAR-1998;	98US-0076621.
XX		
PA	(ICAG-) ICAGEN INC.	

XX	Silvia C, Yu W;
PI	
XX	WPI; 1999-551066/46
DR	P-PSDB; AAY42260.
DR	

PT A new potassium channel alpha subunit, Kir5.1, useful for treating
PT hypertension, acute or chronic renal failure, diabetes insipidus or
PT nephropathy -

PS Claim 4; Page 64-65; 68pp; English.

This sequence represents a human Kir5.1 inward-rectifier potassium channel alpha subunit cDNA. This was isolated and amplified from a human testis cDNA library using PCR primers AA221042 and AA221043. The Kir5.1 alpha subunit is predicted to be approximately 43 kD. The C-terminal tail region (residues 352-383) is divergent with respect to Kir5.1 proteins from other species - for example, there is only 10% identity between the Kir5.1 tail regions of human and rat. Potassium channels are typically formed by four alpha subunits, each with two transmembrane domains, and can be homomeric (made of identical subunits) or heteromeric (made of two or more distinct types of alpha subunits). The human Kir5.1 alpha subunit associates with additional alpha subunits to form a potassium channel which allows potassium influx to a cell, with little potassium outflux (inward rectifier activity). Such inward rectifier potassium channels comprising human Kir5.1 can be heteromeric, containing one or more Kir5.1 alpha subunits, along with other alpha subunits from the Kir family. Kir5.1 can also comprise a homomeric inward rectifier channel. The cDNA can be used to screen for modulators of inward rectifier potassium channels that contain a Kir5.1 subunit, for the treatment of hypertension, acute or chronic renal failure, diabetes insipidus or diabetic nephropathy, hypo- or hyperthyroidism, goitre, hypo- or hyperparathyroidism, pancreatic insufficiency, diabetes, cystic fibrosis, statorrhea, and salivary insufficiency.

Query Match	99.9%	Score 1507.2	DB 20	Length 1509	...
Best Local Similarity	100.0%	Pred. No. 0			
Matches 1509; Conservative	0	Mismatches	0	Gaps	0

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QY	61	agcagcttcatactatcatatgaatgcgcaacaaataccagagctacccgcagagccat	120
Db	61	agcagcttcatactatcatatgaatgcgcaacaaataccagagctacccgcagagccat	120
QY	121	atagctgagaagaagaagcaagaagcagatctactcaacaagaatgtagcgttaatg	180
Db	121	atagctgagaagaagaagcaagaagcagatctactcaacaagaatgtagcgttaatg	180
QY	181	tacttcaagcaacatttttggagaatggggagcatgtgttgacatcttcacaacatt	240
Db	181	tacttcaagcaacatttttggagaatggggagcatgtgttgacatcttcacaacatt	240
QY	241	gtgagacacaagtgaggccataatgtttgataattcttcattatcttcctcgtg	300
Db	241	gtgagacacaagtgaggccataatgtttgataattcttcattatcttcctcgtg	300
QY	301	ttagatattggtcgtcttttttgctcaaaagcttcaacatggcgaatcatataaagat	360
Db	301	ttagatattggtcgtcttttttgctcaaaagcttcaacatggcgaatcatataaagat	360
QY	361	ccagacatcaacccctgtgttgacaacgttcaatcttccaaaggcgctttgtcttc	420
Db	361	ccagacatcaacccctgtgttgacaacgttcaatcttccaaaggcgctttgtcttc	420
QY	421	ctagagaccacaacacacataagataatgttatcgtgtgttactgaagaatgtctgtg	480
Db	421	ctagagaccacaacacacataagataatgttatcgtgtgttactgaagaatgtctgtg	480

[illegible]

RESULT 2
AAD09566
ID AAD09566 standard; cDNA: 1730 BP.
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AC AAD09566;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human transporter and ion channel-15 (TRICH-15) cDNA.
XX
XX Human; transporter and ion channel-15; TRICH-15; cystic fibrosis; mood;
KW gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
KW hypertension; angina; neurological disorder; epilepsy; vaccine; arrhythmia;
KW dementia; depression; Alzheimer's disease; cerebral neoplasm; allergy;
KW Huntington's disease; Parkinson's disease; schizophrenia; polymyositis;
KW demyelinating disease; mental disorder; Schizophrenia; Grave's disease;
KW muscle disorder; cardiomyopathy; catarract; myocarditis; Grave's disease;
KW dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
KW scleroderma; pulmonary artery stenosis; nocturnal; Addison's disease;
KW malabsorption syndrome; hypercholesterolaemia; cancer; ss.
XX
OS Homo sapiens.
XX
FH Key 22..1383
FT CDS
FT
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FT /*product= "Human TRICH-15 protein"
FT 22..117
FT /*tag= b
FT mat_peptide 118..1380
FT /*tag= c
FT /*product= "Mature human TRICH-15 protein"
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PN W0200146258-A2.
XX
PD 28-JUN-2001.
XX
XX 22-DEC-2000; 2000MO-US35095.
XX
XX 23-DEC-1999; 99US-0172000.
PR 14-JAN-2000; 2000US-0176083.
PR 21-JAN-2000; 2000US-0177332.
PR 28-JAN-2000; 2000US-0178572.
PR 02-FEB-2000; 2000US-0179758.
PR 10-FEB-2000; 2000US-0181625.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P,
PI Hillman JL, Azimzal Y, Yue H, Nguyen DB, Yao MG, Gandhi AR,
PI Tang YT, Khan FA;
XX
DR WPI: 2001-418042/44.
DR P-PSDB: AAE04902.
XX
XX Novel human transporter and ion channel proteins useful for treating
PT and preventing transport, neurological, muscle and immunological
PT disorders
XX
PS Claim 5; Page 150-151; 160pp; English.
XX
XX The present sequence is transporter and ion channel-15 (TRICH-15) cDNA.
CC TRICH is used as vaccine. TRICH is useful for treating a disease or
CC condition associated with decreased expression of functional TRICH,
CC such as transport disorder including amyotrophic lateral sclerosis,
CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
CC disease, Duchenne muscular dystrophy, angina and hypertension, bipolar
CC neurological disorders including Alzheimer's disease, amnesia, bipolar
CC disorder, dementia, depression, epilepsy, ischemic cerebrovascular

CC disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
CC disease and Parkinson's disease, demyelinating diseases, mental disorders
CC including mood, anxiety, schizophrenia and seasonal affective disorder,
CC muscle disorder including cardiomyopathy, myocarditis, polymyositis,
CC dermatomyositis, arrhythmias and asthma and immunological disorders
CC including AIDS, adult respiratory distress syndrome (ARDS), allergies,
CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
CC syndrome, systemic lupus erythematosus and other diseases including
CC sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
CC glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
CC psoriasis and viral, bacterial, fungal, helminthic and protozoal
CC infections. TRICH DNA is useful in gene therapy and in diagnostic
CC purposes.
XX
SO Sequence 1730 BP; 520 A; 358 C; 361 G; 491 T; 0 other:

Query Match 95.2%; Score 1436.6; DB 22; Length 1730;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

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DB |||||||
DB ttactactacaactcactccttgatcccttaaggcagcagcaagaatgagctataagc 141

QY 61 agcagctatcatatcatatcatatcagcagcaaaatcccgctaccgccaagacatt 120
DB |||||||
DB agcagctatcatatcatatcagcagcaaaatcccgctaccgccaagacatt 201

QY 121 atagctggaagaagaagaagaagaagaagcattactccaagaatgagcagctgtaatg 180
DB |||||||
DB atagctggaagaagaagaagaagaagcattactccaagaatgagcagctgtaatg 261

QY 202 atagctggaagaagaagaagaagaagcattactccaagaatgagcagctgtaatg 261
DB |||||||

QY 181 tactccaagcacattttggagaaatggggagcattggttgacatctccactctt 240
DB |||||||
DB tactccaagcacattttggagaaatggggagcattggttgacatctccactctt 321

QY 241 gtggacacccaagtgcccatatgtttgataattcttcttataattcttcctg 300
DB |||||||
DB gtggacacccaagtgcccatatgtttgataattcttcttataattcttcctg 381

QY 301 ttgataattggtcgtctcttgggtlcatagccttccatcatcagcagcattataatg 360
DB |||||||
DB ttgataattggtcgtctcttgggtlcatagccttccatcatcagcagcattataatg 441

QY 361 ccagacatcacacttggttgacaagtcacatcttccaaggggcctttgtcttc 420
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DB ccagacatcacacttggttgacaagtcacatcttccaaggggcctttgtcttc 501

QY 421 ctaggagcccaaac 480
DB |||||||
DB ctaggagcccaaac 561

QY 502 ctaggagcccaaac 561
DB |||||||
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DB |||||||
DB ttctggccaacacagtggttagaagaagcagttagaagcccaactctccgcatacaga 801

QY 721 gacagtgaaggagatgacatgacatgacatgacatgacatgacatgacatgacatg 780
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DB gacagtgaaggagatgacatgacatgacatgacatgacatgacatgacatgacatg 861

[illegible]

XX 30-JAN-2001; 2001WO-US00667.
PF
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632166.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236559.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX
XX Example 4; SEQ ID NO: 5079; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell sampl
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
XX
SO Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;

Query Match	Similarity	95.2%	Score	1436.6	DB	22	Length	1921.	
Best Local	Similarity	98.7%	Pred.	No. 0					
Matches	1488	Conservative	2	Mismatches	12	Indels	6	Gaps	4
QY	1	ttactactacaacacacaccttgatcccttaaggccacagcaagaatgagctatacggc	60						
DB	290	ttactactacaacacacaccttgatcccttaaggccacagcaagaatgagctatacggc	349						
QY	61	agcaactatcatattatcaatgcyggaagcaaaatacccaaggtaccgcgcagagacatt	120						
DB	350	agcaactatcatattatcaatgcyggaagcaaaatacccaaggtaccgcgcagagacatt	409						
QY	121	atagcttgagaagagaagaagcaagaagacatttacttccaaagaatgycgcgtgtaatgc	180						
DB	410	atagcttgagaagagaagaagcaagaagacatttacttccaaagaatgycgcgtgtaatgc	469						
QY	181	tacttcaagcacatttttggagaatgcyggaagctatgttgattgacacttccacactct	240						
DB	470	tacttcaagcacatttttggagaatgcyggaagctatgttgattgacacttccacactct	529						
QY	241	gtggacaccaaagtggcgccatagtttgtgataatttcttatacttcttcgcgtgg	300						
DB	530	gtggacaccaaagtggcgccatagtttgtgataatttcttatacttcttcgcgtgg	589						
QY	301	ttgatatattggctcgtctcttttggtcctatagccttccatcagggagactataaatgat	360						
DB	590	ttgatatattggctcgtctcttttggtcctatagccttccatcagggagactataaatgat	649						
QY	361	ccagacatcacaccttgltgttacaacgltccacttcttccacaggggccttttgtctcc	420						
DB	650	ccagacatcacaccttgltgttacaacgltccacttcttccacaggggccttttgtctcc	709						
QY	421	ctagagacccaaacacacacatagatagtgtatcgctgtgttaactgaagaatgctctg	480						
DB	710	ctagagacccaaacacacacatagatagtgtatcgctgtgttaactgaagaatgctctg	769						
QY	481	gccggtgctatggtatcctccagtcacatcttaagtgtgataataatcctttatcatt	540						
DB	770	gccggtgctatggtatcctccagtcacatcttaagtgtgataataatcctttatcatt	829						

```
QY 541 ggagctgccttggcccaaaatggcaactgtcgaagaagagcccaacatcttccagc 600
   |||||||
DB 830 ggagctgccttggcccaaaatggcaactgtcgaagaagagcccaacatcttccagc 889
QY 601 tacttgcaactatagatgtgagagatgggaagcttgcctcatgtgagcatgtgat 660
   |||||||
DB 890 tacttgcaactatagatgtgagagatgggaagcttgcctcatgtgagcatgtgat 949
QY 661 ttctggcccaaacacgtgtgagaagaagatggagcccaacttccgctatacaga 720
   |||||||
DB 950 ttctggcccaaacacgtgtgagaagaagatggagcccaacttccgctatacaga 1009
QY 721 gacagtgaaggagatgacgcatgtcaatlaaagacctcaatlaagtcacagccaatc 780
   |||||||
DB 1010 gacagtgaaggagatgacgcatgtcaatlaaagacctcaatlaagtcacagccaatc 1069
QY 781 atcctgttaccctccggttaactatgtccatgaaattgacacatgagagccctctgtatgcc 840
   |||||||
DB 1070 atcctgttaccctccggttaactatgtccatgaaattgacacatgagagccctctgtatgcc 1129
QY 841 ctggaccgcaaaagcagtaagcaaaagataacttgagatttggtagcatlatactact 900
   |||||||
DB 1130 ctggaccgcaaaagcagtaagcaaaagataacttgagatttggtagcatlatactact 1189
QY 901 ggtgattccacttgaacatctcaccacatctagaagctcctatgttcccgaraatcttc 960
   |||||||
DB 1190 ggtgattccacttgaacatctcaccacatctagaagctcctatgttcccgaraatcttc 1249
QY 961 tggggccataaggtttaatgattcttgggaagttaagaagaagatattacaagaatgaaactgc 1020
   |||||||
DB 1250 tggggccataaggtttaatgattcttgggaagttaagaagaagatattacaagaatgaaactgc 1309
QY 1021 ttacagtttgaagaagatgttgggaagatgtgcccccttggcgtcccaagcaattggagc 1080
   |||||||
DB 1310 ttacagtttgaagaagatgttgggaagatgtgcccccttggcgtcccaagcaattggagc 1369
QY 1081 tggaaagaccacagctccacatagaaaagaccacacagcttgcagaatccctcacgtgc 1140
   |||||||
DB 1370 tggaaagaccacagctccacatagaaaagaccacacagcttgcagaatccctcacgtgc 1429
QY 1141 gacaccaagcgagacgaagatcattagtcgaattgccaattgtagcagcgtgtgaaaa 1200
   |||||||
DB 1430 gacaccaagcgagacgaagatcattagtcgaattgccaattgtagcagcgtgtgaaaa 1488
QY 1201 cccttgaggagaccacacacttgcacacatgagataaggaagaccctatcagaagac 1260
   |||||||
DB 1489 cccttgaggagaccacacacttgcacacatgagataaggaagaccctatcagaagac 1548
QY 1261 tctccctgacttaaacangaatcctctgttgaatcccaaatgttagtcctaaatgtca 1320
   |||||||
DB 1549 tct-cctgactttaaagcag--aatcctgtlagatcccaatgt--agctctaattgtca. 1603
QY 1321 attatgagggttaacacatgaaatcttcttcagccaatcaagtcgttgaacgtgc 1380
   |||||||
DB 1604 attatgagggttaacacatgaaatcttcttcagccaatcaagtcgttgaacgtgc 1663
QY 1381 gctttttgaaggtgttatgggcatgttttatgatalgtctggtagaagtaagaattga 1440
   |||||||
DB 1664 gctttttgaaggtgttatgggcatgttttatgatalgtctggtagaagtaagaattga 1723
QY 1441 aacttggtaaaagataatctaaaatlccatagttctcagttataaattttctctgtc 1500
   |||||||
DB 1724 aacttggtaaaagataatctaaaatlccatagttctcagttataaattttctctgtc 1783
QY 1501 ccggaatt 1508
   |||||
DB 1784 cgcgaatt 1791
```

```
RESULT 4
AAI36580
ID AAI36580 standard; DNA; 1921 BP.
XX
```

```
AC AAI36580;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #5266 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN MO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001: 2001MO-US00663.
XX
PR 04-FEB-2000: 2000US-0180312.
PR 26-MAY-2000: 2000US-0207456.
PR 30-JUN-2000: 2000US-0608408.
PR 03-AUG-2000: 2000US-0632366.
PR 21-SEP-2000: 2000US-0234687.
PR 27-SEP-2000: 2000US-0236559.
PR 04-OCT-2000: 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR.
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID NO 5266; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;

Query Match 95.2%; Score 1436.6; DB 22: Length 1921;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1489; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

QY 1 ttactactcaaaaactactgtgattcccttaaggcacagcaagaatgagattacgyc 60
   |||||||
DB 290 ttactactcaaaaactactgtgattcccttaaggcacagcaagaatgagattacgyc 349
QY 61 agcagctatcataltatcaatgtcgagcgaacaaataccaggtaccccgcaagcacat 120
   |||||||
DB 350 agcagctatcataltatcaatgtcgagcgaacaaataccaggtaccccgcaagcacat 409
QY 121 atagctgagaagaagagcaagaagacgattacttacaagaatgycagctgtaagtc 180
   |||||||
DB 410 atagctgagaagaagagcaagaagacgattacttacaagaatgycagctgtaagtc 469
QY 181 tacttcaagacacatttttggagaatggggaagcctatgtgttgcacttccacactct 240
   |||||||
DB 470 tacttcaagacacatttttggagaatggggaagcctatgtgttgcacttccacactct 529
QY 241 gtgacaccaagtgcgcacatgttgtgatatlttcttatcttatactctctgtg 300
   |||||||
DB 530 gtgacaccaagtgcgcacatgttgtgatatlttcttatcttatactctctgtg 589
QY 301 ttgatatgtgctctgtcttcttggctcatagcttccatcatatggtgcgcatcattaaatgat 360
   |||||||
DB 590 ttgatatgtgctctgtcttcttggctcatagcttccatcatatggtgcgcatcattaaatgat 649
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Oy 361 ccagacatcacacttggtgtgacacagctccatctcttcacagggcctttgtctcc 420
    |||||
Db 650 ccagacatcacacttggtgtgacacagctccatctcttcacagggcctttgtctcc 709
Oy 421 ctgaagaccccaaacacatgagatggtatggtgtgtgtgtgtgtgtgtgtgtgt 480
    |||||
Db 710 ctgaagaccccaaacacatgagatggtatggtgtgtgtgtgtgtgtgtgtgtgt 769
Oy 481 ggcgtgcatggtgcatctccatctccatctcttaagtltcatcataaatacatcttacc 540
    |||||
Db 770 ggcgtgcatggtgcatctccatctccatctcttaagtltcatcataaatacatcttacc 829
Oy 541 ggaagctgcttgcccaaaatggcaactgctcgaaagagagcccaaacatctgcttcagc 600
    |||||
Db 830 ggaagctgcttgcccaaaatggcaactgctcgaaagagagcccaaacatctgcttcagc 889
Oy 601 tactttgacttatagatagatagatggaagcttgcctcatgttgccgcatgtgtat 660
    |||||
Db 890 tactttgacttatagatagatagatggaagcttgcctcatgttgccgcatgtgtat 949
Oy 661 ttccgccaacacacgctgtgtagaagaaagctttagagcccaactctccgtatatacaga 720
    |||||
Db 950 ttccgccaacacacgctgtgtagaagaaagctttagagcccaactctccgtatatacaga 1009
Oy 721 gacagtgaaggagagatgacatggtcatttaagaccctcaaatgtgtcaagccaatc 780
    |||||
Db 1010 gacagtgaaggagagatgacatggtcatttaagaccctcaaatgtgtcaagccaatc 1069
Oy 781 atccggtgcatcccggtgactatgttccatgaaatggacatgaaagccctctgtatcc 840
    |||||
Db 1070 atccggtgcatcccggtgactatgttccatgaaatggacatgaaagccctctgtatcc 1129
Oy 841 cttagccgcaaaagcagtagcacaagataactttagaatlttgtagacttatactact 900
    |||||
Db 1130 cttagccgcaaaagcagtagcacaagataactttagaatlttgtagacttatactact 1189
Oy 901 ggtgattccacttggaacatctccaatctagaagctccatgttcccgaaatcttc 960
    |||||
Db 1190 ggtgattccacttggaacatctccaatctagaagctccatgttcccgaaatcttc 1249
Oy 961 tggggccataggtttaatgagtctcttggaaggttaagaggaatltatacaagtgaatc 1020
    |||||
Db 1250 tggggccataggtttaatgagtctcttggaaggttaagaggaatltatacaagtgaatc 1309
Oy 1021 ttacagtttgaaggaagtgtggaatlatatgccccttlttgagtgccaagaatltgac 1080
    |||||
Db 1310 ttacagtttgaaggaagtgtggaatlatatgccccttlttgagtgccaagaatltgac 1369
Oy 1081 tggaaagacacagcagctccacatagaaaaagcaccacagcttcggaatctccgacgtcg 1140
    |||||
Db 1370 tggaaagacacagcagctccacatagaaaaagcaccacagcttcggaatctccgacgtcg 1429
Oy 1141 gacacaaagcgagagcgaaggtcatttagtgcaattgcatgttcagcgctgtgtaaa 1200
    |||||
Db 1430 gacacaaagcgagagcgaaggtcatttagtgcaattgcatgttcagcgctgtgtaaa 1488
Oy 1201 cccttgaagagaccacacttccgccaacatgaaataggaacaacacttcatcagaagc 1260
    |||||
Db 1489 cccttgaagagaccacacttccgccaacatgaaataggaacaacacttcatcagaagc 1548
Oy 1261 tctccctgacttaaaangaatctctgttwaatcccaaatggttgccttaaatgtga 1320
    |||||
Db 1549 tct-cctgacttlaaacag--aactctgttagaatacccaatgt--agtccttaattgca 1603
Oy 1321 attatgagggcgacacacatcatcttattctttagccaatcaagctgttgaacgctg 1380
    |||||
Db 1604 attatgagggcgacacacatcatcttattctttagccaatcaagctgttgaacgctg 1663
Oy 1381 gcttttttgaaggtgtatggtatgtttatgatgatgctggtgaagtagaagtaagta 1440
    |||||
Db 1664 gcttttttgaaggtgtatggtatgtttatgatgatgctggtgaagtagaagtaagta 1723
Oy 1441 aactgtgtaaaagataatcctaaataatcctatagttctcagttatataaatlttctgt 1500

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Db 1724 aactgtgtaaaagataatcctaaataatcctatagttctcagttatataaatlttctgt 1783
Oy 1501 ccggaatt 1508
    ||||
Db 1784 cgcgaatt 1791

RESULT 5
AAS92631
ID AAS92631 standard; cDNA; 1395 BP.
AC AAS92631:
DT 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #28435.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
PN WO200175067-A2.
PD 11-OCT-2001.
PF 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HWSE-) HXSEQ INC.
PI Drmanac RF, Liu C, Tang YT;
PI WPT: 2001-639362/73.
DR P-PSDB: ABC28444.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1: SEQ ID No 28435; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_ptc_sequences.
XX
SQ Sequence 1395 BP; 410 A; 319 C; 299 G; 367 T; 0 other:

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Query Match 83.5%; Score 1259.4; DB 23; Length 1395;
Best Local Similarity 99.2%; Pred. No. 0;

Matches 1294; Conservative 2; Mismatches 4; Indels 4; Gaps 3;

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QY 1 ttactatacaaacaccacttgatcccttaagggcagcaagaagaatgacttaagc 60
Db 94 ttactatacaaacaccacttgatcccttaagggcagcaagaagaatgacttaagc 153
QY 61 agcagctatcatatatacaatgcgcagcaaaaataccaggtaccgcagagacat 120
Db 154 agcagctatcatatatacaatgcgcagcaaaaataccaggtaccgcagagacat 213
QY 121 atagctgagagaagaagaagaagaagaagaagaagaagaagaagaagaaga 180
Db 214 atagctgagagaagaagaagaagaagaagaagaagaagaagaagaagaaga 273
QY 181 tacttaagaacacatttttgagaatggggaagctatgtgtgacatctcacac 240
Db 274 tacttaagaacacatttttgagaatggggaagctatgtgtgacatctcacac 333
QY 241 gtggacaacaaagtggcgacatagtgtgataattcttatctatattctctg 300
Db 334 gtggacaacaaagtggcgacatagtgtgataattcttatctatattctctg 393
QY 301 ttgatttttgctctgtctttttgctcatagcctttcatatcatgtgcattaa 360
Db 394 ttgatttttgctctgtctttttgctcatagcctttcatatcatgtgcattaa 453
QY 361 ccagacatacacaccttggtgtgacaacgtccattcttcacagggcctttgt 420
Db 454 ccagacatacacaccttggtgtgacaacgtccattcttcacagggcctttgt 513
QY 421 ctagaagaacccaacacacatagatatgtgtatgcgtgtgttactgagaag 480
Db 514 ctagaagaacccaacacacatagatatgtgtatgcgtgtgttactgagaag 573
QY 481 ggcgtgtcatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 574 ggcgtgtcatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 633
QY 541 ggaagctgcttggcacaacatgacactgtctgaaagaacccaacacatctg 600
Db 634 ggaagctgcttggcacaacatgacactgtctgaaagaacccaacacatctg 693
QY 601 tacttgacattatagatagatagatagatagatagatagatagatagatag 660
Db 694 tacttgacattatagatagatagatagatagatagatagatagatagatag 753
QY 661 ttctggcacaacacacgtgtgagaagaacagtttagagcccaacttccgtat 720
Db 754 ttctggcacaacacacgtgtgagaagaacagtttagagcccaacttccgtat 813
QY 721 gacagtgaaaggagatgacatgacatttaagaacccaacttaagtccaagc 780
Db 814 gacagtgaaaggagatgacatgacatttaagaacccaacttaagtccaagc 873
QY 781 atccctggtaaccccgtaactatgtccatgataatgacatgagaagccctgt 840
Db 874 atccctggtaaccccgtaactatgtccatgataatgacatgagaagccctgt 933
QY 841 ctggacacgaacagtagacagaagaagaagaagaagaagaagaagaagaaga 900
Db 934 ctggacacgaacagtagacagaagaagaagaagaagaagaagaagaagaaga 993
QY 901 ggtgattccactggaacatccacacatcagaagccctatgtcccgaraattc 960
Db 994 ggtgattccactggaacatccacacatcagaagccctatgtcccgaraattc 1053
QY 961 tggggccataagtttaatgattcttggaaagttaagaagaagaagaagaaga 1020
Db 1054 tggggccataagtttaatgattcttggaaagttaagaagaagaagaagaaga 1113
QY 1021 ttacagtttgaagaagtggtgagaatataatgcccccttttgcagtgccaag 1080
Db 1114 ttacagtttgaagaagtggtgagaatataatgcccccttttgcagtgccaag 1173

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QY 1081 tggaaagaccagcagctccacatagaaaagcaccacagttcgagaatctgcagtcg 1140
Db 1174 tggaaagaccagcagctccacatagaaaagcaccacagttcgagaatctgcagtcg 1233
QY 1141 gacacaaagcgagacgaaggtcattagtgcagttgcattgcagcagctgtgaaa 1200
Db 1234 gacacaaagcgagacgaaggtcattagtgcagttgcattgcagcagct-gtga 1292
QY 1201 cccctgaggaagaccacacttgcgcacatagatataggaagaacactatagaagc 1260
Db 1293 cccctgaggaagaccacacttgcgcacatagatataggaagaacactatagaagc 1352
QY 1261 tctccctgactttaaacaagaatcctctgtgacatcccaatgt 1304
Db 1353 tct-cctgactttaaacaag--aatctctgtagaatcccaatgt 1393

RESULT 6
AAF85049
ID AAF85049 standard; DNA; 1257 BP.
XX
AC AAF85049;
XX
DT 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a human Kir5.1 polypeptide.
XX
KW Kir5.1; inwardly rectifying potassium channel; ion channel;
KW renal failure; hypokalemia; hypertension; hypotension; thyroid disease;
KW pancreatitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1257
FT 1257
FT /tag= a
FT /product= "Kir5.1"
XX
PN WO200125258-A1.
XX
PD 12-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US26996.
XX
PR 04-OCT-1999; 99US-0157491.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Swanson RJ, Liu Y, McKenna E;
XX
DR WPI: 2001-290604/30.
XX
DR P-PSDB; AAB68275.
XX
PT Novel nucleic acid encoding human Kir5.1 subunit protein useful for
PT identifying activators and inhibitors of potassium channels containing
PT the protein subunit useful for treating various diseases
XX
PS Claim 3; Fig 1; 52pp; English.
XX
CC The present sequence encodes a human Kir5.1 subunit protein. Kir5.1
CC is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
CC are useful for identifying inhibitors or activators of potassium
CC channels. Kir5.1 proteins are useful as attractive targets for drug
CC discovery and as valuable research tools for understanding ion channel
CC biology. Kir5.1 proteins are also useful for identifying inhibitors or
CC activators of potassium channels. Inhibitors or activators screened
CC using Kir5.1 protein are useful for treating a variety of diseases
CC involving excessive or insufficient potassium channel activity, such as
CC renal failure, hypokalemia, hypertension, hypotension, thyroid disease
CC and pancreatitis.
XX
SQ Sequence 1257 BP; 358 A; 287 C; 276 G; 336 T; 0 other;

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Query Match 80.5%; Score 1214.4; DB 22; Length 1257;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1249; Conservative 2; Mismatches 4; Indels 4; Gaps 3;

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QY 46 atgagcttaccgagcagcgtatcatattatcaatgcygagcgaataatccaggtac 105
DB 1 atgagcttaccgagcagcgtatcatattatcaatgcygagcgaataatccaggtac 60
QY 106 ccgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 165
DB 61 ccgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
QY 166 ggcagctgtaagcttacttcaagcagcagcagcagcagcagcagcagcagcagc 225
DB 121 ggcagctgtaagcttacttcaagcagcagcagcagcagcagcagcagcagcagc 180
QY 226 atcttaccactctgtgtgacacacagctgtgtgtgtgtgtgtgtgtgtgtgtgt 285
DB 181 atcttaccactctgtgtgacacacagctgtgtgtgtgtgtgtgtgtgtgtgtgt 240
QY 286 tatattctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 345
DB 241 tatattctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
QY 346 gattatataatgatacacaacacacacacacacacacacacacacacacacacac 405
DB 301 gattatataatgatacacaacacacacacacacacacacacacacacacacacac 360
QY 406 gcttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 465
DB 361 gcttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
QY 466 gaaagaatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 525
DB 421 gaaagaatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
QY 526 aataccattatcatgtgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 585
DB 481 aataccattatcatgtgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
QY 586 accattcggttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 645
DB 541 accattcggttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
QY 646 tggcgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 705
DB 601 tggcgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
QY 706 ctccgctatacagaagacagtgaaagagagagagagagagagagagagagagagag 765
DB 661 ctccgctatacagaagacagtgaaagagagagagagagagagagagagagagagag 720
QY 766 gtcaacgacacaaatcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 825
DB 721 gtcaacgacacaaatcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
QY 826 aagcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 885
DB 781 aagcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
QY 886 acaattatcatatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 945
DB 841 acaattatcatatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
QY 946 ccccgagaaatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1005
DB 901 ccccgagaaatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
QY 1006 tacaagaatgaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1065
DB 961 tacaagaatgaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020

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```

QY 1066 gccaaagcattgtgactgtgaaagaccagcagctccacatagaaagaccagcagcttgcga 1125
DB 1021 gccaaagcattgtgactgtgaaagaccagcagctccacatagaaagaccagcagcttgcga 1080
QY 1126 gaatcctgcagcttcgacacacagcagcagcagcagcagcagcagcagcagcagc 1185
DB 1081 gaatcctgcagcttcgacacacagcagcagcagcagcagcagcagcagcagcagc 1140
QY 1186 agcagctgtgtgaaaccccgagagagacacacacacacacacacacacacacacacac 1245
DB 1141 agcagctgtgtgaaaccccgagagagacacacacacacacacacacacacacacacac 1199
QY 1246 accattacagaagccttccctgtacttlaacangaatcctctgtgtgtgtgtgtgtgt 1304
DB 1200 accattacagaagccttccctgtacttlaacangaatcctctgtgtgtgtgtgtgtgt 1255

RESULT 7
AAK17807
ID AAK17807 standard; DNA; 1118 BP.
XX
AC AAK17807;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 17798.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00067.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 17798; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;

```

Query Match 70.9%; Score 1069.6; DB 22; Length 1118;
 Best Local Similarity 99.9%; Pred. No. 9; 7e-302;
 Matches 1069; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


```

QY 301 ttgatattgctctctcttcttgctcacaagcttccatccatgagcagatcattaaatgat 360
Db 349 ttgatattgctctctctcttcttgctcacaagcttccatccatgagcagatcattaaatgat 408
QY 361 ccagaacatcacactctgtgtgacaagctccatctctcacaagggccttttctctcc 420
Db 409 ccagaacatcacactctgtgtgacaagctccatctctcacaagggccttttctctcc 468
QY 421 cttagagaccacaacacacataagatagtatgctgtgtgtacccagaagaatgtctctg 480
Db 469 cttagagaccacaacacacataagatagtatgctgtgtgtacccagaagaatgtctctg 528
QY 481 gccgtgctcattgctgctcctcagctccatctcttaagtctgcatcataaataccttaccat 540
Db 529 gccgtgctcattgctgctcctcagctccatctcttaagtctgcatcataaataccttaccat 588
QY 541 ggaagctgcttgcccaaaaatgagcaactgctcgaaagagagcccaacatctgcttcagc 600
Db 589 ggaagctgcttgcccaaaaatgagcaactgctcgaaagagagcccaacatctgcttcagc 648
QY 601 tacttgctcattatagatgagatggaagcttgcctcattgtgagcagcttgat 660
Db 649 tacttgctcattatagatgagatggaagcttgcctcattgtgagcagcttgat 708
QY 661 ttccggccaacacacgctgtgtagaagagcaagcttagagcccaactctccgctatacagaa 720
Db 709 ttccggccaacacacgctgtgtagaagagcaagcttagagcccaactctccgctatacagaa 768
QY 721 gacaaatgagagagatgagatgagctttaaagaccccaattgttcaagcacaacatc 780
Db 769 gacaaatgagagagatgagatgagctttaaagaccccaattgttcaagcacaacatc 828
QY 781 atccgtgacaccccgctgaactatgtccatgaatgtgacacagagagccctctgtatgac 840
Db 829 atccgtgacaccccgctgaactatgtccatgaatgtgacacagagagccctctgtatgac 888
QY 841 cttagacgcaaaagcagctgacaaagataacttggatctgtgtgacattatctataact 900
Db 889 cttagacgcaaaagcagctgacaaagataacttggatctgtgtgacattatctataact 948
QY 901 ggtgctcactgagacatctcacaactctagaagctctctatgctcccgagaaatcttc 960
Db 949 ggtgctcactgagacatctcacaactctagaagctctctatgctcccgagaaatcttc 1008
QY 961 tggggccataggtttaatgatgtctcttggaagttaagaggaagctattacaagaatgacatgc 1020
Db 1009 tggggccataggtttaatgatgtctcttggaagttaagaggaagctattacaagaatgacatgc 1068
QY 1021 ttacagttgaaagagagctgtggaagctatgaccccttgcagctgacaa 1070
Db 1069 ttacagttgaaagagagctgtggaagctatgaccccttgcagctgacaa 1118

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RESULT 9

AAF85050 standard; cDNA: 1257 BP.

AAF85050;

09-JUL-2001 (first entry)

Nucleotide sequence of a rat Kir5.1 polypeptide.

Kir5.1: inwardly rectifying potassium channel; ion channel;

renal failure: hypokalemia; hypertension; hypotension; thyroid disease;

pancreatitis; ss.

Rattus sp.

Key Location/Qualifiers

CDS 1..1257

FT /*tag= a

```

FT /product= "Kir5.1"
FT /note= "no termination codon given"
PD MO200125258-A1.
PD 12-APR-2001.
PF 29-SEP-2000; 2000MO-US26996.
PR 04-OCT-1999; 99US-0157491.
PA (MERI ) MERCK & CO INC.
PI Swanson RJ, Liu Y, McKenna E;
DR MPI: 2001-290604/30.
DR P-PSDB: AAB68277.
XX
XX
XX Novel nucleic acid encoding human Kir5.1 subunit protein useful for
XX identifying activators and inhibitors of potassium channels containing
XX the protein subunit useful for treating various diseases
XX
XX Disclosure: Fig 4A-B: 52pp; English.
XX
XX The present sequence encodes a rat Kir5.1 subunit protein. Kir5.1
XX is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
XX are useful for identifying inhibitors or activators of potassium
XX channels. Kir5.1 proteins are useful as attractive targets for drug
XX discovery and as valuable research tools for understanding ion channel
XX biology. Kir5.1 proteins are also useful for identifying inhibitors or
XX activators of potassium channels. Inhibitors or activators screened
XX using Kir5.1 protein are useful for treating a variety of diseases
XX including excessive or insufficient potassium channel activity, such as
XX renal failure, hypokalemia, hypertension, hypotension, thyroid disease
XX and pancreatitis.
SQ Sequence 1257 BP; 325 A; 325 C; 314 G; 293 T; 0 other:

Query Match 57.6%; Score 869.6; DB 22; Length 1257;
Best Local Similarity 82.6%; Pred. NO. 2.5e-243;
Matches 1030; Conservative 1; Mismatches 211; Indels 5; Gaps 3;

QY 46 atgagctattacgagcagcagctatattatcaatgcgagcagcaaataccagagctac 105
Db 1 atgagctattacgagcagcagctatattatcaatgcgagcagcaaataccagagctac 60
QY 106 ccgcagagcacattatgagctgagaagagagaagagcagcttacttccaaaagat 165
Db 61 ccgcagagcacattatgagctgagaagagagaagagcagcttacttccaaaagat 120
QY 166 ggaagctgtaaatgtctacttcaagcacatlttgagaagatggagagctatgtgtgac 225
Db 121 ggaagctgtaaatgtctacttcaagcacatlttgagaagatggagagctatgtgtgac 180
QY 226 atcttcacacactctgttgacaacagtgagcagatgtgtgtatatttcttacc 285
Db 181 atcttcacacactctgttgacaacagtgagcagatgtgtgtatatttcttacc 240
QY 286 tatattctctgtgtgataatttgctcgtcttggctatgaccttataatgac 345
Db 241 tatattctctgtgtgataatttgctcgtcttggctatgaccttataatgac 300
QY 346 gatcattaaatgacacagacacacactgtgttgacaacagctccatcttccaaag 405
Db 301 gatcattaaatgacacagacacacactgtgttgacaacagctccatcttccaaag 360
QY 406 gccctttgttctccctagagacccaacacacatagatatgtatcgtgtgtact 465
Db 361 gccctttgttctccctagagacccaacacacatagatatgtatcgtgtgtact 420
QY 466 gaagaatgtctgtgagcgtgtgtatgtgatacccccagctcatcttaagtgtgacata 525

```

Db	421	gaagaatgcctcttgccgcgctgcgaagctcatcttcagttccatctctgactgcatcacta	486
Oy	526	aataccttcatcttgagagctgcctcttgcccaaatgycaatctgtcgaagaagaccocaa	585
Db	481	aacaccttcatcttgaggagcctcttgcaaaagatgycgaccgccggaagcgaagccag	540
Oy	586	acacattgcttcgcactcttgacacttaagtaagagagatgaggagccttgctcatg	645
Db	541	acacatccgcttcgactatttcgcacactatccgcatgtagagagaggaaccttgctccatg	600
Oy	646	tggcgacatggtatattcttgccaaaccacggtgtagaaggagacagttaaaggcccaact	705
Db	601	tggcgacatggtatattcttgccaaaccacggtgtagaaggagacagttaaaggcccaact	660
Oy	706	ctccgcctatcagaagaacagtgaagaagagatgacatgacatgtcttaagaagctcaatta	765
Db	661	ctggtgcatcttcagaagaacagcgaagaaggcggatggaagatggtgtttaaagaacctcaatc	720
Oy	766	gtcaaacgaccaatcatcatctgtgtcacaccgcggtaactatgtlcatgtaaatgtgacaatg	825
Db	721	gtcaatgaccgagataatccgtgtaacgacgagacatgtgcataagaaattgaccacag	780
Oy	826	agccctctgtatgaccttgacgcgcaaaagcagtagccaaagaataacttgagatttggtg	885
Db	781	agtcctctgtatgaccttgacgcgcaaaagcagtagccaaagaataacttgagatttggtg	840
Oy	886	acattatctcatactgtgattccctactgtaaacatatctcaccaatctagaagctcctatggt	945
Db	841	acattatctcatactgtgactctactactggaatccacccagttccagaagtctctaagtc	900
Oy	946	ccccgataaattctcttgggggcctaaagttaatgatgtcttggaaggttaagaagaatg	1005
Db	901	ccccgataaattctcttgggggcctaaagttaatgatgtcttggaaggttaagaagaatg	960
Oy	1006	tacaaagtgcacgcgtctacaggtttggaaggaaatgtggaagatatagcgcccctttgcagt	1065
Db	961	tacaaagttaacgtctgtccaggttttgggggaagcgtggaagtttaacgcccctttgcagt	1020
Oy	1066	gcccaagaatttgatctggaagaaagccacgcagctccaca---tagaaaaagcaccacagtt	1122
Db	1021	gcccaacaactgtagcttggaagagccacacagctcacaacacttgtagaaaaagctccctgc	1080
Oy	1123	cggagaatctgcagcgttcgagacaccaaagcgaagacgaagtgcaattagtgcagttgcca	1182
Db	1081	cggagaatctgcagcgttcgagacaccaaagcgaagacgaagtgcaattagtgcagttgcca	1140
Oy	1183	gtcgcgcgcgtggtgaaaacaccttgagagacccacacatttcgcacaacttgatatagga	1242
Db	1141	gtgcgcgcgcgt-gtgcgaacaccagagagacgcagcgttccccaagaatgtgagtgaa	1199
Oy	1243	aacaccttcatcagaagcgttccctctgacttaacataaangaatcctctg	1289
Db	1200	gtctccctatcagaagaagcct-ctgcactttaaagcagatctccaag	1245

RESULT	10
AA35739	
ID	AA35739 standard; cDNA; 907 BP.
XX	
AC	AA35739;
XX	
DT	09-JUL-1999 (first entry)
XX	
DE	cDNA encoding a protein identified by the signal sequence trap method.
XX	
KW	Signal sequence trap method; SSF method; immunisation; inhibition;
KW	infection; allergy; cancer; regulation; tissue formation; tissue repair;.
KW	activin activity; inhibin activity; chemokine activity;
KW	cytokine activity; blood coagulation regulation; agonist; antagonist;
KW	metabolic disorder; hormonal disorder; immune disorder;
KW	severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
KW	wound; SS.
XX	

OS Homo sapiens.
XX
PN W09918126-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98WO-JP04514.
XX
PR 07-OCT-1997; 97JP-0274674.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Fukushima D, Shibayama S, Tada H;
XX
DR WPI: 1999-277254/23.
XX
P-PSDB: AAY02380.
XX
PT Polypeptides identified by the signal sequence trap method from a
XX human cDNA library
XX
PS Claim 4; Page 213-215; 281pp; Japanese.
XX

CC AAX35656335747 represent cDNA sequences that encode novel polypeptides
CC (AAV02358-84) which are identified from a human placental cDNA library
CC by the signal sequence trap (SST) method. The polypeptides have a
CC broad range of physiological activity, including immunisation against
CC and inhibition of infections, allergies and cancer; regulation of tissue
CC formation and repair; activin/inhibin activity; chemokine/cytokine
CC activity; blood coagulation regulation; and receptor/ligand agonist
CC or antagonist activity. The polypeptides can be used for prevention
CC and treatment of disorders including infections by bacteria, yeasts and
CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;
CC immune disorders (including severe combined immunodeficiency (SCID)
CC and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
XX
SQ Sequence 907 BP; 278 A; 210 C; 183 G; 236 T; 0 other;

[illegible]

XX Human diagnostic and therapeutic polynucleotide (DITHP) #102.
 DE Human: receptor; diagnostic: therapeutic; gene therapy; vaccine;
 XX cell proliferative disorder; Crohn's disease; lymphoma; leukemia;
 KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;
 KW respiratory disorder; ss.
 XX Homo sapiens.
 OS
 XX WO200162927-A2.
 PN
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US06059.
 XX
 PR 24-FEB-2000; 2000US-0184693.
 PR 24-FEB-2000; 2000US-0184697.
 PR 24-FEB-2000; 2000US-0184698.
 PR 24-FEB-2000; 2000US-0184768.
 PR 24-FEB-2000; 2000US-0184769.
 PR 24-FEB-2000; 2000US-0184770.
 PR 24-FEB-2000; 2000US-0184771.
 PR 24-FEB-2000; 2000US-0184772.
 PR 24-FEB-2000; 2000US-0184773.
 PR 24-FEB-2000; 2000US-0184774.
 PR 24-FEB-2000; 2000US-0184775.
 PR 24-FEB-2000; 2000US-0184777.
 PR 24-FEB-2000; 2000US-0184797.
 PR 24-FEB-2000; 2000US-0184813.
 PR 24-FEB-2000; 2000US-0184837.
 PR 24-FEB-2000; 2000US-0184841.
 PR 24-FEB-2000; 2000US-0185213.
 PR 24-FEB-2000; 2000US-0185216.
 PR 12-MAY-2000; 2000US-0203785.
 PR 13-MAY-2000; 2000US-0204228.
 PR 16-MAY-2000; 2000US-0204525.
 PR 16-MAY-2000; 2000US-0204821.
 PR 16-MAY-2000; 2000US-0204908.
 PR 16-MAY-2000; 2000US-0205232.
 PR 17-MAY-2000; 2000US-0204815.
 PR 17-MAY-2000; 2000US-0204863.
 PR 17-MAY-2000; 2000US-0205221.
 PR 17-MAY-2000; 2000US-0205285.
 PR 17-MAY-2000; 2000US-0205286.
 PR 17-MAY-2000; 2000US-0205287.
 PR 17-MAY-2000; 2000US-0205323.
 PR 17-MAY-2000; 2000US-0205324.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
 PI Chen A, D'Sa SA, Amshney S, Dahl CR, Dam TC, Daniels SE;
 PI Dutour GE, Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AL,
 PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A;
 PI Wright RJ, Yap PE, Yu PE, Bradley DL, Bratcher SR, Chen W;
 PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
 XX
 DR WPI: 2001-502867/55.
 DR P-PSDB: AAU19516.
 XX
 PT polynucleotides encoding diagnostic and therapeutic proteins, e.g.,
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics
 PT
 XX
 PS Claim 1: Page 340-341; 522pp; English.
 XX
 CC The invention relates to polynucleotides (I) encoding diagnostic and
 CC therapeutic (DITHP) polypeptides (II), which include e.g., enzymes, (I)
 CC and proteins involved in growth and development and receptors (II) and
 CC (II) may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate DITHP expression. For example, (I) and
 CC (II) may be used to treat disorders associated with decreased polypeptide

CC expression by rectifying mutations or deletions in a patient's genome,
 CC that affect the activity of the DITHPs, by expressing inactive proteins
 CC or supplementing the patient's own production of them. (I) and (II)
 CC may be used to treat diseases, for example, cell proliferative disorder,
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
 CC leukemia, autoimmune disorders, and respiratory disorders. Additionally,
 CC (I) may be used to produce the DITHPs, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. (I) and
 CC its complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. (II) may also be used as antigens in the production of DITHP
 CC antibodies against DITHPs and in assays to identify modulators of DITHP
 CC expression and activity. The anti-DITHP antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-DITHP
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of DITHPs in samples (e.g., by enzyme linked immunosorbent
 CC assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and
 CC therapeutic (DITHP) polynucleotides of the invention.
 XX
 SQ Sequence 856 BP; 240 A; 192 C; 177 G; 247 T; 0 other;
 Query Match 28.5%; Score 430; DB 22; Length 856;
 Best Local Similarity 100.0%; Pred. No. 4.4e-115;
 Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ttactactacaaactacacctgataccttaaggcagcagcaagaatgagctatacggc 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 427 ttactactacaaactacacctgataccttaaggcagcagcaagaatgagctatacggc 486
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 agcagctacatattatcattcgaatgcgagcgaataatccagcgctaccgcagagccatt 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 487 agcagctacatattatcattcgaatgcgagcgaataatccagcgctaccgcagagccatt 546
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 atagctgagaagaagaagaagaagaagaacgattacttaccagaatgagcagctgtaatg 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 547 atagctgagaagaagaagaagaagaagaacgattacttaccagaatgagcagctgtaatg 606
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 tacttcaagaacatttttgagaatgaggaagctatggttgacattccactctt 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 607 tacttcaagaacatttttgagaatgaggaagctatggttgacattccactctt 666
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 gtaggacaccagtgagccatattgttgataatttcttactatattctctcgtgg 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 667 gtaggacaccagtgagccatattgttgataatttcttactatattctctcgtgg 726
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 ttgataattgctctgctcttttgagcattatgcattcattcattcattcattcatt 360
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 727 ttgataattgctctgctcttttgagcattatgcattcattcattcattcattcatt 786
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 ccagacatcacacctgtgttgaacaagtcacattcttcaaggggcctttgtctcc 420
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 787 ccagacatcacacctgtgttgaacaagtcacattcttcaaggggcctttgtctcc 846
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 ctgagagacc 430
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 847 ctgagagacc 856
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 13
 AAH21453
 ID AAH21453 standard: DNA; 1264 BP.
 XX
 XX AAH21453:
 XX
 XX 18-SEP-2001 (first entry)
 XX
 XX Human IRK1 DNA.
 DE
 XX Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
 KW activator; ds.
 KW
 XX

XX Claim 4: SEQ ID NO 14435; 530bp; English.
PS
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging, the
CC monitoring and prognosis diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

Query Match 20.2%; Score 304.4; DB 22; Length 1310;
Best Local Similarity 59.0%; Pred. No. 2.5e-78;
Matches 584; Conservative 1; Mismatches 387; Indels 18; Gaps 3;

QY 142 agaagacgacttactcaaaagatgagcgtgaatgctactcaagcaaatlttga 201
DB 156 aggagccgcttctgaagaagaatgagcactgaatgtcattcaatcatgtggtgag 215
QY 202 gaattgggaagctatgtgtgctacattcactcttctgagaccaaagtggccat 261
DB 216 aaggggaaagcgtgaccccgagacatcttaccacgtgtgtgacatcgtgcggtg 275
QY 262 atcttgatgatttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 321
DB 276 atgctggtatctcttgcgcgtcttcttcttcttcttcttcttcttcttcttctt 335
QY 322 tggctaatgacttcaatcgtgacgatctaatatgacccagacacactgtgtt 381
DB 336 tggctaatgacttcaatcgtgacgatctaatatgacccagacacactgtgtt 395
QY 382 gaaacacgcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 441
DB 396 tcgagtgacacagcttcaagcgtcttcttcttcttcttcttcttcttcttcttctt 455
QY 442 ggaatggtatcgtctgttcttcttcttcttcttcttcttcttcttcttcttctt 501
DB 456 ggtatggtatcgtctgttcttcttcttcttcttcttcttcttcttcttcttctt 515
QY 502 cagtcacatcttaagttgacataaatacattatcattgagcgtccttggccaagt 561
DB 516 cagtcacatcttggcgtgacatcagtcattcattcattgagcgtccttggccaagt 575
QY 562 gcaactgctgaaagagagcgaacacattcgttgcacttcttgcattatagatg 621
DB 576 gcaagcgaagaaagagagacgtcttcttcttcttcttcttcttcttcttcttctt 635
QY 622 agagatgggaagcttgcctcattggtcgcatgtgatttcggccaacacgtgta 681
DB 636 agagatgggaagcttgcctcattggtcggtggtggtggtggtggtggtggtggtg 695
QY 682 gaaagacagttgagcccaacttctcgtacatacagaagacagtggaaggaag--atg 738
DB 696 gaaagacagttgagcccaacttctcgtacatacagaagacagtggaaggaag--atg 755
QY 739 agatggtcatttaagacccaat-----agtaacgacccaatcatctg 766
DB 756 ccccttgatcaataagacccaatggtggtggtggtggtggtggtggtggtggtggtg 815
QY 787 gtaccccggttaactatgtcattgaatgacatagagcgtcgtctgtccctgac 846
DB 816 gtgtcccaatcactatgacatgaatgataagagacgtccttattatgttgaat 875
QY 847 cgcgaagcagtagccaaagataacttggagatttggtagcattatcatatcgtgtg 906

DB 876 aaacagacattgacaacgacgacttgaatcgtgtcattactggaagcattgtgaa 935
QY 907 tcaactggaacattcccaatcagaagcttccatgttcccgaraatttcttgggc 966
DB 936 gccactgccaatgagacacagtgccgtgacttcttactagaacaaatccttctgggc 995
QY 967 catggttcaatgtcttcttgaagttgaaggaagatcacaagtggaactgttaccag 1026
DB 996 caccgcatgagcctgtgcttcttgaaggaagacacacacacaaagtgtgacttccag 1055
QY 1027 ttgaaggaagtggtgaagt--atagcccttcttgcagtgccaaagcattgactgg 1083
DB 1056 ttccacaacttgaagtgcccaacaccccttcttcttcttcttcttcttcttctt 1115
QY 1084 aagaccagcagctcccatagaaaagca 1113
DB 1116 aagaataatattccttcaaatgcaattca 1145

RESULT 15

AAK17341
ID AAK17341 standard; DNA; 1310 BP.
XX
AC AAK17341;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 17332.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001MO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR.
XX
DR WPI; 2001-483446/52.
XX
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX
PS Example 4: SEQ ID NO: 17332; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

Query Match 20.2%; Score 304.4; DB 22; Length 1310;
Best Local Similarity 59.0%; Pred. No. 2.5e-78;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 01:30:25 ; Search time 1703.75 seconds
(without alignments)
11954.163 Million cell updates/sec

Title: US-09-623-304A-2
Perfect score: 1509
Sequence: 1 ttactactacaacacacc.....ttttcttcttcggaattc 1509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569.4	37.7	858	10	BI143740 602907395
2	506.8	33.6	781	10	BI144257 602907822
3	456.4	30.2	710	10	BF780854 602105743
4	452.2	30.0	606	9	AI636030 1292403.X
5	439.6	29.1	753	10	BI143982 602908077
6	431.4	28.5	662	10	BI101237 602886939
7	429.4	28.5	686	10	BI101492 602887284
8	401	26.6	721	9	AM475637 un96409.Y
9	374.8	24.8	783	10	BF789666 602105381
10	374.4	24.8	516	10	BF411612 UI-R-BT1-
11	368.8	24.4	658	9	BB625105 BB625105-
12	354	23.5	641	9	BB643863 BB643863-
13	353.8	23.4	665	10	BF789809 602105362
14	340.6	22.6	461	12	AQ222870 HS_2014-A
15	330	21.9	527	10	BF194884 708902.X
16	330	21.9	651	9	BB644922 BB644922
17	314.6	20.8	1001	10	BI546348 603188840

18	308.6	20.5	690	10	BI101289
19	297.8	19.7	641	9	BB622505 BB622505
20	295.8	19.6	533	9	AM226791 AM226791
21	294.4	19.5	599	9	AM318913 AM318913
22	292.8	19.4	525	9	AI227094 AI227094
23	277.4	18.4	398	9	AI747352 AI747352
24	277	18.4	278	12	B59110 B59110
25	269.8	17.9	740	9	AV602053 AV602053
26	266.8	17.7	575	9	AV603377 AV603377
27	264.6	17.5	484	9	AA989815 AA989815
28	261.6	17.3	899	10	BF780894 BF780894
29	249.8	16.6	2462	11	AK017299 AK017299
30	249	16.5	442	9	AM259025 AM259025
31	249	16.5	645	9	AI788269 AI788269
32	247.4	16.4	493	9	AM259349 AM259349
33	247.4	16.4	526	9	AM012077 AM012077
34	226.2	15.5	411	9	AV603376 AV603376
35	226	15.0	349	9	AM475246 AM475246
36	226	15.0	753	12	CNS03W7V CNS03W7V
37	219.4	14.5	433	9	BB848349 BB848349
38	218	14.4	702	10	BI553872 BI553872
39	215.2	14.3	1110	10	BF789199 BF789199
40	209.4	13.9	430	12	AQ245235 AQ245235
41	208.4	13.8	494	12	A2825911 2M0101B19
42	205.4	13.6	444	9	AM318491 AM318491
43	189.6	12.6	336	9	AI271845 AI271845
44	185.6	12.3	687	9	AI647481 AI647481
45	180	11.9	780	10	BI100286 BI100286

ALIGNMENTS

RESULT 1
LOCUS BI143740 858 bp mRNA linear EST 05-JUL-2001
DEFINITION 602907395F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5064407
ACCESSION BI143740
VERSION BI143740
KEYWORDS BI143740.1 GI:14603741
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1173 row: n column: 24
High quality sequence stop: 854.

FEATURES

source

1. 858
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5064407"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. 1"
BASE COUNT 227 a 220 c 201 g 210 t

Db 489 ACGGTTACCGCTGTGTACCGAAGAGTGTCTGTGTGCTGTACTGACAGTATCCTTCAGT 548
Qy 506 ccaatctaatgcatcataaataacttatacttgaagagctgtggtgcgaatagga 565
Db 549 CCATCTCTACGCTGCATCATTAACACCTTCATCTATGTGAGAGCGCTTGGCAAAATGGCAA 608
Qy 566 ctgtcgaagaagagccaaacattcgttctagctacttctgcatatagatagag 625
Db 609 CTCGCGGGAAGAGAGCGACAGACCATACGCTTACGCTATTTTGGCCCATTTGGTATGAGAG 668
Qy 626 atgggaagctt- gectcatgtggcgatgtgattcttcggccaaacacagtgtagaa 664
Db 669 ACGGGAGGCTTGGCTCATGTGTGGCCCATAGTGTGATCTCCGACAAACCATGTGTAGAG 728
Qy 685 ggaacagtagagcccaacttcctcgctat 714
Db 729 GGCACGGGTGAGAGCCCACTTCTGCGCTAT 758

RESULT 3
BF780854 710 bp mRNA linear EST 12-JAN-2001
DEFINITION BF780854 602105743p1 NCI-CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223626
5', mRNA sequence.
ACCESSION BF780854
VERSION BF780854.1 GI:12085887
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 710)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC).
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM9812 row: f column: 11
High quality sequence stop: 703.
Location/Qualifiers
1. 710
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223626"
/clone_11b="NCI-CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library. 1"
BASE COUNT 198 a 177 c 177 g 158 t
ORIGIN

Query Match 30.2% Score 456.4 DB 10; Length 710;
Best Local Similarity 83.5% Pred. No. 8.6e-102;
Matches .552; Conservative 1; Mismatches 103; Indels 5; Gaps 3;

Qy 624 agatgggaagcttgcctcaatgtggtgcatactgtgattcttcggccaaacacagtgtaga 683
Db 1 AGAGGGGAGAGCTTGGCTCATGTGTGGCGCATAGTGTGACTTCCGACCAACCATGTGTAGAG 60
Qy 684 aggaacagtagagcccaacttcctcgcatatagagaagacagtgaggagtagagat 743
Db 61 GGGCAGCGTGAAGGCCCACTTCTGCGCTATTCAGAAAGACAGTGAAGGAGGAGTGAAGAT 120

Qy 744 ggcattaaagacctcaaatatagtcacagaccacaaatcatccttgctgaccggtaactat 803
Db 121 GGGCTTTAAAGACCTCAAACTGCTCAATGACAGATTAATCTGGTAACTCAATGACTAT 180
Qy 804 tgcataatgaatgcacatagagagccctcgtatgtcccttgaccggaagcaatagcaaa 863
Db 181 TGTCATTAATGAATGACATGAGAGCCCTGCTGTATGCGCTTGACCGGCAAGGCAATGGCCAA 240
Qy 864 agataacttgagatttggtagcattatctactgtgaltccacttggaacatctca 923
Db 241 AGATAATTTTCGAGATTCTGCTGACATTATTTATCTGATGGATTCCACTGGGACATCCCA 300
Qy 924 ccaattagaagctcctaagtctcccgaraaatctcctggtggccataggttaatatgt 983
Db 301 CCAGTCAGAGATTCTCTACATCCCGACAGAAATTTCTGTGGGCGACAGATTTATATATGT 360
Qy 984 ctgtgaagtltaagagagatlatcaaaagtgaactgcttatacagtttgaaagagtaga 1043
Db 361 ATTGGAAGTGAAGAGAAAGTACTACAAAGTGAAGTCACTCTTGCACTTTGAAGGAAGCTGCA 420
Qy 1044 agtataagccccccttggcagtgcccaagaaatgagctggaagacagagctccaca- 1102
Db 421 AGCTACAGCCCTCTTGTGAGTCCCAAACTGAGCTGGAAGGACCAACTCAACAA 480
Qy 1103 --tagaaaagacacccacagcttcgagaatcctgcagctggaacccaagcgagagag 1160
Db 481 CTGGAGAAACCTCCCTGCGAGAGATCTGCAATTTGTGACCAACCAACCGAGGGG 540
Qy 1161 gtcaatagtgacagtgccatgtgcagcagctgtgtgaaacccctggagagaccacact 1220
Db 541 GTCTTCAAGCGCATGTGTGCTGTGTGACAGACT-CTGAGAAACCAAGAGAGACCGCTCTGT 599
Qy 1221 tgcgcacatgacatataagggaacacactatcagaagctctccctgacttaaacang 1280
Db 600 CCCCACAGATGATGATGAGAGATGCTCCATCAGAAACCCCT-CCGTACTTTAATATAG 658
Qy 1281 a 1281
Db 659 A 659

RESULT 4
A1636030 606 bp mRNA linear EST 16-DEC-1999
LOCUS A1636030/c
DEFINITION t292a03.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296012 3'
similar to SW:IRRX_RAT P52191 INWARD RECTIFIER POTASSIUM CHANNEL
B1R9 ;, mRNA sequence.
ACCESSION A1636030
VERSION A1636030.1 GI:4687360
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 606)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE Tumor Gene Index
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/btpr/image/image.html
Insert Length: 681 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 446.

FEATURES
Source
Location/Qualifiers
1. 606
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2296012"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 175 a 125 c 111 g 191 t 4 others
ORIGIN

Query Match 30.0%; Score 452.2; DB 9; Length 606;
Best Local Similarity 95.3%; Pred. No. 9e-101;
Matches 506; Conservative 1; Mismatches 18; Indels 6; Gaps 4;

OY 964 ggcataagtttaatgattgcttggaagtaagagaagattacaagtgactgtcta 1023
|||||
DB 606 GCCATAGGTTAATGATGCTTTGGAAGTTAAGAGAAATTAACAGTGAAGTCTAA 547
OY 1024 cagtttgaaggaagtgtagatataatgcccccttttggaagtgccaagaatttgactg 1083
|||||
DB 546 CAGTTTGAAGGAAGTGTAAGTATATGCGCCCTTTTGAGTGCCAAAGCAATTTGAGCTGG 487
OY 1084 aagagccagcaactcacatagaaagacacacagttcgagaactcgtcacgtcgagc 1143
|||||
DB 486 AAGAGCAGACAGCTCCACATGAAAAAGACACAGTTCGAGAAATCCGACAGCTGGAGC 427
OY 1144 accaagcgagagaagagtcattagtcagttgcaattgtcaagagctggtgaaaccc 1203
|||||
DB 426 ACCAAGCGGAGAGCAAGGTCATTTAGTGCAGTTGCATGTGACAGCT-GTGAAGAACCC 368
OY 1204 tgagaagaccacactttcgacacacatgatatagagggaacacacttacaagaactct 1263
|||||
DB 367 TGAGGAGACACACCTTCGCGCACATGAAATATAGGAAACACCTTATCAAGAACTCT 308
OY 1264 ccctgacttaacangaactcctctgtgwaatcccaagtgtaagtccttaaatggcaat 1323
|||||
DB 307 -CCTGACTTTAAACAGAAAT--CTCTGTAGAAATCCAAATGT--AGTCCTAATTTGCAAT 253
OY 1324 atgaaggtactacatgaatcattatccttcagccaatcaagtcgtgtgaaacgtgact 1383
|||||
DB 252 ATGAGGGGACACCACTGAATCATTTATCTTTTCAGCCAAATCAAGTCGTGTAACCGTGC 193
OY 1384 tttttgaagtgcttgatgctatgtttttagatgagtgctgggaaggaagtgtaagtaac 1443
|||||
DB 192 TTTTGAAGAGTGTATGCTATGTTTATGATGATGCTGGTGAAGTGAAGTAAAC 133
OY 1444 ttggttaaaagatacctaaatcctcatagttcctcagttattaaatttt 1494
|||||
DB 132 TTGGTAAAGATATCTAAATTCATAGTCTCAGNTATTATTAATTTT 82

RESULT 5
B1143982 753 bp mRNA linear EST 05-JUL-2001
LOCUS 602908077E1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5065051
DEFINITION 5', mRNA sequence.
ACCESSION B1143982
VERSION B1143982.1 GI:14603983
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 753)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNL11175 row: 1 column: 20
High quality sequence stop: 725.

FEATURES
Source
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5065051"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. I"

BASE COUNT 212 a 166 c 171 g 204 t
ORIGIN

Query Match 29.1%; Score 439.6; DB 10; Length 753;
Best Local Similarity 81.9%; Pred. No. 1.2e-97;
Matches 531; Conservative 0; Mismatches 114; Indels 3; Gaps 2;

OY 26 ccctaaggcacagaagaatgagctattacggcagcagctatcatatcatgagcg 85
|||||
DB 107 CCTAAGGACCAAGCAAGAAATGAGCTATTACGAAAGTGTACAGAGATTGCAATGTGG 166
OY 86 acgcaaatatcaccagagctcccgccagagacacattatagctgagaagaagaaga 145
|||||
DB 167 ACTCCAAATATCCAGAGCTATCTCCAGACATGCCATCTGAGAGAGAAAGCAGAA 226
OY 146 gacgattactcacaagaatgagcagctgtaatgctacttcaagcacattttgagaat 205
|||||
DB 227 GCGGCTTGCTCCACAAGATGACAGCTGTAATGTACTTTAAACATTTTGGAGAT 286
OY 206 ggggaagctatgtgtgacatcttcaaccactctgttggaacccaagtgtgacatagt 265
|||||
DB 287 GGGGAGCTACATGTGTGATTTTATTTTACCACTCTGTGATACCAAGTGGCCCATATGT 346
OY 266 ttgtgatttcttattatctatctctcgtgtgtgtgattgattgctgtcctgtgc 325
|||||
DB 347 TCATATATTTTCTCTGCTTACATTTCTCTCGGTGATATTTGGTTTCATATTTTGGC 406
OY 326 taatagccttcatcagtgagctatctaatatgattccagacatcacaacctgtgtgaca 385
|||||
DB 407 TCATACCTTTTATCAGCAGACGATTAAGCATACCAATATACACCCCTTGTTGTTGACA 466
OY 386 acgtccatcttctcagagggcctttgtctcctccatagagacccaaccacatagat 445
|||||
DB 467 ACGTGATTCATTTACGCGCTGATTTTATCTCCCTGAGACCCAGACACCATTTGGAT 526
OY 446 atggtatcgcgtgtgtactgaagaatgtctgtgagcggtcactagtgatccccaat 505
|||||
DB 527 ACGGTTACCGCTGTGCACGAAGAGTGTCTGTGCTTACTAGACAGTATCTTCAAT 586
OY 506 ccatcttaagttgacatcaataatacttataatitggaagctgcttggtgccaatgagcaa 565
|||||
DB 587 CCATCTCAGCTGCATCAAAACACCTTATCATTTGAGACACGCTTGGCAAGATGGCAA 646
OY 566 ct--gtcgaagaagagcccaaaccaattcgtttcagctacttgcactatagtagtag 623

Db 647 CTGGCCGGAAGAGAGACGACCATTAAGCGTTGAGTATTGGCCCTCATGATGAG 706
QY 624 agatgggaagcttgcctcatgtgagcgaatgttgatcttcggcaca 671
Db 707 AGACGGGGAAG-TTGGCTCATGTGGGGAATAGGTGAATTCGACCA 753

RESULT 6
LOCUS B1101237 662 bp mRNA linear EST 26-JUN-2001
DEFINITION 60286639f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042480
5', mRNA sequence.
ACCESSION B1101237
VERSION B1101237.1 GI:14552130
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 662)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1M1116 row: m column: 09
High quality sequence start: 24
High quality sequence stop: 660.
Location/Qualifiers
1..662
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="5042480"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 160 a 168 c 152 g 182 t
ORIGIN

Query Match 28.6%; Score 431.4; DB 10; Length 662;
Best Local Similarity 83.3%; Pred. No. 1.2e-95;
Matches 539; Conservative 0; Mismatches 101; Indels 7; Gaps 4;

QY 192 cattttggaagaatgggaagcatgtgtgacatcttcacacactgtgtgacacaa 251
Db 16 CACTCTTGAGAGATGGGAGGACATGATGATTTTACACCTTGATGAGATCA 75
QY 252 gtggcgacatcatgtgtatattcttctatctatctctcgtgtgtatattgg 311
Db 76 GTGGGCCCATATGTTGATATATTTCTGTCTGTATCATTTCTCTGTTGATTTGG 135
QY 312 ctctgtcttggcctatgaccttcatcatatgacatctatataatgacagacac 371
Db 136 TTCCATATTTTGGCTCATAGCTTTCATCAGGAGACATTAAGGATCCAGATATCAC 195
QY 372 aactgtgtgcaagatcatcttcttcacagggcctttgttctccctagaagacca 431
Db 196 CCTTGTGTGACAAAGCTGATTCATTCAGGCTGCATTTTATTCCTCGAGACCA 255
QY 432 aaccacatagatatgtatcgcgtgttactgaagaatgttctgtgscgtgtcat 491

Db 256 GACCACCATGTGATAGGTTACCGCTGTGCACGGAAGTGTCTGTGGCTGTACTGAC 315
QY 492 ggtgatctccatccatcttaagtgtcatcataaacttataatcatgtgagcctt 551
Db 316 AGTGAATCTTCAATCCATCTCTAGCTGATCATCAATCAACCTTCATGATGAGACGCTT 375
QY 552 gggcaca-atggaaactgtctgaaagagcccaaccttctgttcaactatttgcac 610
Db 376 GGCCAAAGATGCGAATGCGCCGGAGAGAGCCGACACATACCTTCACCTATTTTGCCC 435
QY 611 ttaagtatgaga--gagtggaagcttgcctcatgtgagcgtatgttctcgcc 668
Db 436 TCATTTGATGACACGACGGAACGCTTTCCTCATCTGCGCATAGGTGACTTCGAC 495
QY 669 aaacacggtgtagaagaacagtagag---cccaactctccgtatatacagaagacag 725
Db 496 AAACCATGTGTCAGAGGACGCTGACAGGCCACACCTTCTGCTATTCAGAAAGACAG 555
QY 726 tgaaggagagatgacatgtgcatlta-aagacctcaatattgacacgacccaatcatcc 784
Db 556 TGACGGGAGAGTACGATGCGCTTACAAAGACCTCAAACTCGTAATGACAGATATATCC 615
QY 785 tgtcaccccgtaactatgttcatgaaatgtacatgagacccct 831
Db 616 TGTGTAATCTCAGTACTATTTGTCATGACATTTGACATGAGACCT 662

RESULT 7
LOCUS B1101492 686 bp mRNA linear EST 26-JUN-2001
DEFINITION 602867284f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042372
5', mRNA sequence.
ACCESSION B1101492
VERSION B1101492.1 GI:14552385
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 686)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1M1116 row: h column: 21
High quality sequence stop: 684.
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone_image="5042372"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 194 a 155 c 150 g 187 t
ORIGIN

Query Match 28.5%; Score 429.4; DB 10; Length 686;
Best Local Similarity 83.5%; Pred. No. 3.8e-95;

Matches	487	Conservative	0	Mismatches	96	Indels	0	Gaps	0
QY	26	ccctaaggcaacgaagaatagcatttaagcgagcagcattcatatlatcatatcg	85						
Db	89	CCCTTAAGGACCAAAAGAAATGACCTATTACGGAATGATCAGAGATGTCAATGTGG	148						
QY	86	acgcaaataccaggtcaccgccgagacacattatagctgagaagaagaaga	145						
Db	149	ACTCAAAATATCCAGGCTATCTCTCCAGACATGCCATCGCTAGAAAGAAAGCAGAGA	208						
QY	146	gaagattacttcacaaagatggcagctgtaatgcttaacttcaagacatttggagaat	205						
Db	209	GGCGCTGTGTCACAAAGATGGCAGCTGTAAGTGTACTTTAAACATTTTGGAGAT	268						
QY	206	ggggagacatgtagttagacatcttcacacactctgtgagacaagtagggcatalgt	265						
Db	269	GGGGAGAGCTACATGGTTGATATTTTACCACCTTGTGGATACCAAGTGGCCATATGT	328						
QY	266	ttagatatttcttattatattatctctctgtggttagatattgtctgtcttggc	325						
Db	329	TCATATATATTTCTCTGTCCTTACATTCCTCTCGTGTGATATTTGGTCCATATTTAGC	388						
QY	326	tatagcctttcatatgtagcgtatctataaagatccagacatacacttggttgaca	385						
Db	389	TCATAGACCTTTTATATACGGAGACTATTAAAGGATACAGATATACACCCCTTGTTGACA	448						
QY	386	acgtcacctcttcacaaggcgcccttctctcccttagagacccaacacatagat	445						
Db	449	ACGTGATTCATTATTACGGCTGATTTTATTTCTCCTGGAGACCAGACACCATTTGAT	508						
QY	446	atggttatcgtcgtgttactgaagaatgtctcgtggccgtgctcatgltgacctcag	505						
Db	509	ACGGTTACCGCTGTGTACACGGAAGTGTCTGTGTGCTGTACTGACAGTATCTTCAGT	568						
QY	506	ccatcttaagttgcacataaaactcttatcatcttggagctccttgcccaaatggcaa	565						
Db	569	CCATCTCAGCTGCATCATTAACACCTTGTATATTGGACAGGCTTTGGCAAGATGGCA	628						
QY	566	ctgctcgaagaagagcccaacattcgttcaagctacttgc	608						
Db	629	CTGCCCGAAGAGAGACCCAGACCATACGCTTACGATATATTCG	671						
RESULT	8								
LOCUS	AM475637	721 bp	mRNA	linear	EST 24-FEB-2000				
DEFINITION	un99d09.y1 Sugano mouse kidney mR1A Mus musculus cDNA clone IMAGE:5220017.5, similar to U7:092307.092307 INWARDLY RECTIFYING POTASSIUM CHANNEL KIR5.1, mRNA sequence.								
ACCESSION	AM475637								
VERSION	AM475637.1	GI:7045743							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.								
AUTHORS	1 (bases 1 to 721)								
	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Person								
	Underwood,K., Steptoe,M., Theisling,B., Allen,M., Bowers,Y., Person								
	,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter								
	,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,								
	Waterston,R. and Wilson,R.								
	The WashU-NCI Mouse EST Project 1999								
TITLE	Unpublished (1999)								
JOURNAL	Contact: Marra M/WashU-NCI Mouse EST Project 1999								
COMMENT	Washington University School of Medicine								
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA								
	Tel.: 314 286 1800								
	Fax: 314 286 1810								
	Email: mouseest@wustl.wustl.edu								
	This clone is available royalty-free through LBL; contact the								
	IMAGE Consortium (info@image.llnl.gov) for further information.								
	MG1:1018741								

```
Trace considered overall poor quality
Seq primer: custom primer used
High quality sequence stop: 1.
    Location/Qualifiers
        1. .721
FEATURES
    source
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BASE COUNT	208 a	176 c	179 g	158 t
ORIGIN	sequencing: 5' end primer CTTCTGCTCTATAAGCTCG and 3' end primer CGACCTGCAGCTCGAGACA.			

Query Match	Similarity	26.5%	Score	401	DB	9	Length	721
Best Local Match	Similarity	75.8%	Pred.	3.9e-88				
Matches	521	Conservative	1	Mismatches	161	Indels	4	Gaps
QY	582	ccaacacatcgtctcagcactactctgcactctataggtatgagagatcgtggaagcttgcct	641					
Db	1	CCACACCATACGCTTGAGCTATATAGCCGCCATCTGGGGGTAGTGACCGGATCGCTCTCT	60					
QY	642	catgtgcgcatttggtaatttttggccaaccacgtgtgtagaagaacgcttaagggcca	701					
Db	61	CATGTGGGCGATAGGATACCTTCGCACCAACATGTGGGGGAAGGCACGTAGAGGCCA	120					
QY	702	actctccgcctacagagaacagtgtgaagggagatgacatgcatgtcattaaagactcaa	761					
Db	121	ACTTATGTGGCTATTCCACAGACATAGAGAGGAGGATGACCATGCGCTTTAAGACTCCA	180					
QY	762	atagtaacaagcaacaatcabcctgtgtcaccgccgttaactatgttccatgtaaattgacca	821					
Db	181	ACTGCTCAGTACACAGATAGTAAAGCCCTGGTAACTCCAGGAGACTATGTGTCCATGAATAGACCA	240					
QY	822	tgaagagccctctgtatctccctcttgaacccgaagacagctagccaagaataactttgagattt	881					
Db	241	TGAGAGCCCTTGAAATGCGCTGGACCCGAAGGCAAGTGGCCAAAGATTAATTACGACAGCTT	300					
QY	882	ggtgacatttactctactactgtgtgatttccacttggaaacatctcaccaaactagaagctctca	941					
Db	301	GGTGACATATATATATCTGTGTGATTCACATGGGACATCCACACAGTCCAGAAAGTTCTTA	360					
QY	942	tgttccccgaraanactctctctgggggcataaggtttaaatagtctcttggaaagttaagaagaa	1001					
Db	361	CATCCCCGAGAAATTTCTCTGGGGCCACAGGTTTCTGATGATTTTGAAGTAAAGTAAGGA	420					
QY	1002	gtatacaaaagtgaacgctctacagctttgaaggaagtgtgtgaagatactgccccctttg	1061					
Db	421	GTACTACAGGTGAACCTGTTGCACTGTTGAAGAGACAGGGAAATTCTACGCCCGCTTTTG	480					
QY	1062	cagttgccaaagaatctgagcttgaagaagccagcagctctccaca---tagaaaacaccacac	1118					
Db	481	CAGTCCCAAAACAACCTGGAGCTGTAGAGCCGACACAACGTCACAACTTGAAGAAAACGCGCC	540					
QY	1119	agttcgagaatccctcgcaactctcgagacccaagcgagagaagaagtcatctagtgcagttgc	1178					
Db	541	TGCCGAGAGATTCACATTTCTGACACCAACACCATGATGCTCTCTCCATTGAGGCAATTTCC	600					

QY	1179	catcttcagcagcctgctgttaaaacccctggagagaccacccactctgcgcacacatgaataa	1238
DB	601	CCTGGTGAACACT-CTGTAACCCATATGAAACCGATCTGTCCACACAGATGATGTG	659
QY	1239	gggaacacctatcagaagctctcc	1265
DB	660	AAGATATGCTCTATCAGATATCATCTGC	686
RESULT	9		
LOCUS	BF789666	783 bp	mRNA linear EST 12-JAN-2001
DEFINITION	60210528JF1 NCI_CGAP_Kid14 Mus musculus cdna clone IMAGE:4223157		
ACCESSION	BF789666		
VERSION	BF789666.1	GI:12094702	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 783)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@mail.nih.gov		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LLM9811 row: b column: 22		
	High quality sequence stop: 721.		
FEATURES	Location/Qualifiers		
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	/strain="FVB/N"		
	/db_xref="taxon:10090"		
	/clone_image="4223157"		
	/clone_lib="NCI_CGAP_Kid14"		
	/lab_host="DH10B (TI phase-resistant)"		
	/note="Organ: Kidney; Vector: pCMV-SPO6; Site: 1; Note:		
	Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.75 kb. Constructed by Life		
	Technologies. Note: This is a NCI_CGAP Library. I"		
BASE COUNT	216 a	176 c	181 g
ORIGIN			210 t

	Query Match	Similarity	24.8%	Score	374.8	DB	10	Length	783
	Best Local	Similarity	79.3%	Pred. No.	1	le=81			
	Matches	520	Conservative	0	Mismatches	127	Indels	9	Gaps
Oy	26	cccttaaggcaacgcaagaatgagctattacggcagcagcatcatcatatcaatgcgg	.85						
Db	127	cccttaaggacccaanaagaatgagctattacgggaagtgcatacagatgttccaaatgtg	186						
Oy	86	acgcaanaataccagagctaccgccagagcacattlaagtctagaagaagaagacaaga	145						
Db	187	actccaatatccaggcttccctccagacacatccctctctgagagacagacaagcaaga	246						
Oy	146	gacgattactcaacaagaatgcaagctgaatgctcactcaagaacatttttgagaat	205						
Db	247	ggcggcttgctccacaaagatgscagctgtaatgtgtaactttaaacacatttttggagaa	306						
Oy	206	ggggaagctatgttgattgacatctcacaactctgtgtgacaacaaagtgcgcacatgt	265						
Db	307	ggggagcgtacacatgattgatttttttacccactctgttgatccaagtgagccgacataatg	366						

FEATURES	SOURCE
<p>1. 516</p> <p>Location/Qualifiers</p> <p>/organism="Rattus norvegicus"</p> <p>/strain="Sprague-Dawley"</p> <p>/db_xref="taxon:10116"</p> <p>/clone="UI-R-BT1-dmp-d-10-0-UI"</p> <p>/clone_1id="UI-R-BT1"</p> <p>/dev_stage="adult"</p>	<p>266 10</p> <p>LOCUS Bf411612/c</p> <p>DEFINITION Bf411612 516 bp mRNA linear EST 28-NOV-2000</p> <p>ACCESSION UI-R-BT1-dmp-d-10-0-UI.s1 UI-R-BT1 Rattus norvegicus CDNA clone Bf411612</p> <p>VERSION Bf411612.1 GI:11399601</p> <p>KEYWORDS EST.</p> <p>ORGANISM Rattus norvegicus</p> <p>SOURCE Norway rat.</p> <p>COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.</p> <p>REFERENCE 1 (bases 1 to 516)</p> <p>AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.</p> <p>TITLE Normalization and subtraction: two approaches to facilitate gene discovery</p> <p>JOURNAL Genome Res. 6 (9), 791-806 (1996)</p> <p>MEDLINE 97044477</p> <p>COMMENT Contact: Soares, MB</p> <p>Program for Rat Gene Discovery and Mapping</p> <p>University of Iowa</p> <p>451 Eckstein Medical Research Building Iowa City, IA 52242, USA</p> <p>Tel: 319 335 8250</p> <p>Fax: 319 335 9365</p> <p>Email: msoares@blue.weeg.uiowa.edu</p> <p>The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized mid-brain library cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)</p> <p>Seq primer: M13 Forward</p> <p>POLYA=yes.</p>

Query March 24.4%. Score 368.8 : DB.9; Length 658:
Best Local Similarity 82.9%: Pred. No.3.2e-80;
Matches 421: Conservative 0; Mismatches 87; Indels 0; Gaps 0

Dy 26 cccttaaggcacaagaagatgagtactataacgcagacgatcatatlatcaatgcgg 85
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 cccrtaaaagaccacaagaagatgacctattttaggaagtgctnacaaganctcattgtcg 209
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Oy 86 acgcaaatatcccaggtctacccgccagagcacattataagctcyagaagaagaagacaaga 145
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Db 210 actccaatatctccagacgtatccctccagagcaccatcccttcagaaagacaaagaaa 269
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Oy 146 gacgattacttcacaagaatggcagcttaatgcttaacttcagacacatttttggaaat 205
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Db 270 gcccttgcctccacaaagatggcagactgtaatgtgtactttaaacacatttttggaaat 329
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Oy 206 gggaagactatgttgtacacatctaccactctgtgagaccaagltgycgcatalgt 265
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Db 330 gggaagactatgttgtacacatctaccactctgtgagaccaagltgycgcatalgt 389
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Oy 266 ttgtgatttttttcttacttatatctctctgtgtgtatatttggcttgcctttggc 325
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Db 390 tctgaatatattttcttctgtcttaacatttctctctgtgtgtatatttggcttgcctttggc 449
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Oy 326 tcataagcttcatcatgtgagatctatcttaaagatccacaacacacacttgtgtgaca 385
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Db 570 acggttaccgcctgtgttaccgaaagtgctctggggcttgtgtgacagtgatcttccaat 629
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Oy 506 coactctaagtgtacatcataaataactt 533
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Db 630 ccattctcagctgcatctaaacacacctt 657
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
BB643863 LOCUS B643863 641 bp mRNA linear EST 31-AUG-2001
DEFINITION BB643863 RIKEN full-length enriched, adult male corpora
quadrigenima Mus musculus cdna clone B230120P21 5', mRNA sequence.
ACCESSION BB643863
VERSION BB643863.1 GI:15402155
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 641)
Arakawa,T., Carrinci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A,
'Hizomo,K., Horii,F., Isilli,Y., Ito,M., Kawai,J., Konno,H., Koude
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tadamu,I., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email:genome-res@gsc.riken.go.jp.

```
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsubiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y.,kira,A. and
Hayashizaki,Y.
RIKEN Integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichipillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh.M., Carninci,P., Sugahara
,X. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Yamanaka,I., Kitayama,H., Kondo,S., Saito,T., Shingana,A., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata.K., Atakawa,T.,
Ishii.Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. 641
/organism="Mus musculus"
/db_xref="taxon:10090"
/cdname="B230120P21"
/clone_id="RIKEN full-length enriched, adult male corpora
quadrigemina"
/sex="male"
/tissue_type="corpora quadrigemina"
/dev_stage="adult"
/lab_host="DH10B"
/note=Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research group in Riken
Genomic Sciences Center and Genome Science laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGACGAGAGAAGATCCCAAGACTCTTTTGTGGTTTTTTTTCVN 3'] , cDNA was
prepared by using trehalase thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGCGAAGCATTCGCAGTAATAATTAAATATCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
PLC I."
BASE COUNT 176 a 142 c 145 g 178 t
ORIGIN
Query Match 23.5% Score 354, DB 9, Length 641:
Best Local Similarity 82.7%; Pred. No. 1.de-076;
Matches 405; Conservative 0; Mismatches 85; Indels 0; Caps 0;
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OY	206	ggggaagatctgtagtctaacacctccacacctctgtgaaagccaaatgagggccataatgt	265
Db	332	ggggagcgtacacgttatgtatatt	391
OY	266	ctgtgataatcttcttatacctataatctctcgtgtgataattggtctgtctctttggc	325
Db	392	tctgtaatt	451
OY	326	tcaatagccttcaatcatatgagcatctatttaaaatgatacagacatacactctgtgttgca	385
Db	452	tcataatgaccttttcatatcagagacacatatttttttttttttttttttttttttttttt	511
OY	386	acgttcattctcttcaagagggcccttttctgtctctccctagagaagccaaaccacataagat	445
Db	512	acgttcatt	571
OY	446	atggtctacgcctgttctactgaaagatcttctgtgacgctgtctcatgtgtatcctccaat	505
Db	572	acggttaccgcctggcgctacccgaaagatgctctgtggggctgtactgacccggagatcccttagt	631
OY	506	ccatctctaa	515
Db	632	ccatctcttag	641

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RESULT 13
BF789809 LOCUS 665 bp mRNA linear EST 12-JAN-2001
DEFINITION 602105362p1 NCI_CGAP_Kid4 Mus musculus cDNA clone IMAGE:422390
5', mRNA sequence.
ACCESSION BF789809
VERSION BF789809
KEYWORDS BF789809.1 GI:12094845
SOURCE EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 665)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: L149811 row: 1 column: 15
High quality sequence stop: 617.
Location/Qualifiers
1..665
FEATURES
source

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/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone IMAGE:4223390"
 /clone_id="NCL_CGAP_Kid14"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: kidney; Vector: pCMV-Sport6; Site.1: NotI;
 Site.2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCL_CGAP library. |"
 194 a 146 c 144 g 180 t 1 others

Query Match	23.4%;	Score 353.8;	DB 10;	Length 665;
Best Local Similarity	82.4%;	Pred. NO. 1.6e-76;		
Matches 453;	Conservative	0;	Mismatches 93;	Indels 4;
			Gaps	4;

Oy	26	cccttaaggagcaagaagaatgaacctcttaaggaagagatcatcatcttaaatcgaag	85
Db	101	cccttaaggaccagaaagaatgaacctctttacggaagagctactacagagattttcatatgcg	160
Oy	86	acgcaaaataccaggatgcctcccgagagacatlatagcttgaaagaagaagcaagaa	145
Db	161	actccaaattatccagagctatctctccagagcattggccatctgcgtagaaagagacaaagaa	220
Oy	146	gaagatctactcacaagaatgycagctgtaatgctactcttaagcacattttggagaat	205
Db	221	ggcggcttctccacaaagatggcacctgtaattgtgtactttaaacacatttttggagaaat	280
Oy	206	ggggaagctatggtgtgacaatccaccacactctgtgagacaaagatgagccatatgt	265
Db	281	ggggagagctaacatggttatattttttaccactcttgtgataccaaagtcggcccatatgct	340
Oy	266	ttgtagataattcttactatatactctcgtgtgtgataattggtctgctctttggc	325
Db	341	tcataatattttttctgtctttacattttctctctgtgtatatttggttcataattttggc	400
Oy	326	tcataagccttcatcatatgagcatctataataatgatccagacatacaacactgtgtttgaca	385
Db	401	tcattagcctttcatcacacgagacactatttaaacgacccagaaatatacccccttgctg-tgcaca	459
Oy	386	acgtccactctcttccaggggcctttgtgtctccctccagagaaacccaacacataagat	445
Db	460	acgtcatttcatattttacggcctgcattttttattctcccttggaagaccagaccacatttgcat	519
Oy	446	atggtctacgcctgttactgaagaatgtctctgtgagccgtgtca-tgtgtatccctcaag	504
Db	520	acggtttacccggctgctacccgaagagctcctgtggtgctgtactgacagntgattccttcag	579
Oy	505	tcacatttaagttgcatcataataacacttatacttgaagctgctgcctgtggccaatatgca	564
Db	580	ttccattccctcag-tgcattcatataa-acctttcatcatattggagccagacccttggaataatgggc	637
Oy	565	actgctgcaa 574	
Db	638	atggcccgaa 647	

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
14	A022870		A022870	A022870									
		HS_2014_A2_H08_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2014 Col=16 Row=O, DNA sequence.	A022870	A022870.1	GI:3636483	GSS.	Homo sapiens human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	"1 (bases 1 to 461)	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	J. Mol. Biol.	99380589	
													Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 2014 row: O column: 16 Class: BAC ends High quality sequence stop: 461. Location/Qualifiers

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source 1. 461
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/db_xref="taxon:9606"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 136 a 102 c 106 g 117 t
ORIGIN

Query Match 22.6%; Score 340.6; DB 12; Length 461;
Best Local Similarity 96.7%; Pred. No. 2.7e-73;
Matches 357; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

OY 637 tgcctatgtgcgcattggtgatttcggccaaccagtgtagaaggaacagtttaga 636
DB 2 TGCCTATGTGGCGCATGTGTGATGTGCGCCAAACACGCTTGTAGACGACAGTTAGA 61
OY 697 gcccaactctccgctatcacagaagacagtgaggagagatgcagtgcatttaagac 756
DB 62 GCCCACTTCTCGCTATACATAGACAGTGAAGGAGATGACATGCGATTTAAGAC 121
OY 757 ctcaattagtcacgacacaaatcctcctgaccccgtaactatgtgccatgaat 816
DB 122 CTCGAATTAATCAACGACCAAAATCATTTGTCACCCCGGAACATTTGCCATGAAT 181
OY 817 gacatgagaagccctctgcatgacctgacccgaagcagtagccaaagataacttga 876
DB 182 GACCATGAGAGCCCTGTATGCTTGAACCCGATAGCAGTATCAAGTAACCTTGAG 241
OY 877 atttgtagacattatcctactgtgattgcacgtggaacatcctacacatagaagc 936
DB 242 ACTTGTGTCATTTATCTATACGTGATTCACCTGGAACATCTACCATTTAAGC 301
OY 937 tccatgttcccccgaataatctctcggggccaaagagtttaagtgtcttggaagta 936
DB 302 TCCATATGTTCCCGAGAAATTTCTGAGCCATAGGTTAATGATGTCTGGAAG- 360
OY 997 aggaagat 1005
DB 361 AGCAAGTAT 369

RESULT 15
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LOCUS BF194884 708902.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3643634 3'
DEFINITION similar to TR:092307 Q92307 INWARDLY RECTIFYING POTASSIUM CHANNEL
KIR5.1; mRNA sequence.
ACCESSION BF194884
VERSION BF194884.1 GI:11081177
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 527)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
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FEATURES High quality sequence stop: 475.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3643634"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with
a modified polylinker. Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502853). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 162 a 106 c 93 g 166 t
ORIGIN

Query Match 21.9%; Score 330; DB 10; Length 527;
Best Local Similarity 95.3%; Pred. No. 1.1e-70;
Matches 382; Conservative 1; Mismatches 12; Indels 6; Gaps 4;

OY 1108 aagcgcccccagttcgagaatctctcagtcgacccaagcgaggaagtcattt 1167
DB 527 AAGGACACACCAATGTGAGATCTGACGTCGACACCAAGCGAGACCAAGTCAATT 468
OY 1168 agtgcagttgccattgcagcagctgtgaaacccctgaggagacacacacttcgca 1227
DB 467 AGTGCAGTTGCCATTGTGACGACACT-GTGAAMCCTGAGAGACCAACCACTCCGCCAC 409
OY 1228 acatgaataaggaaacacacttatacagaagctctccctgactttaaacangaatcctc 1287
DB 408 ACATGAATATAGGGAACACCTTATGAGAAAGCTCT-CTGACTTTAAACAG--AATCTC 352
OY 1288 tgtwgaatcccaatcttagtcctaaatgtcaattatgaggctacacactgatactt 1347
DB 351 TGTAGATCCCAATGT--AGTCTTAATTTGCAATTTAGAGGCTACCACTGATATTT 294
OY 1348 tatcttcagccaatcaagtcgtgtgaacgltgcttlttgaaagtgtatgctatgt 1407
DB 293 TATCTTCAAGCCAAATCAAGTCGTGTAACGTCGCTTTTGAAGGTATGCTATGT 234
OY 1408 ttatgatgatgctggtgtagtagtaagtaaaacttggtlaaagaataactaaat 1467
DB 233 TTTATGATGATGCTGCGGTAAGTAGACTTAAGTTAACTTGTAAGAATATCTAAATAAT 174
OY 1468 ccatagttccagttatlaaattttctgttcgggaatt 1508
DB 173 CCATAGTCTCAGTATTAATAATTTTCTGTCGCCAATT 133
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Search completed: October 5, 2002, 03:59:14
Job time: 8929 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 02:43:00 ; Search time 53.33 Seconds
(without alignments)
6950.327 Million cell updates/sec

Title: US-09-623-304A-2
Perfect score: 1509
Sequence: 1 ttactactacaacacacc.....ttttctgttcggaattc 1509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/CTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfills1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280.4	18.6	2310	1 US-08-461-690B-1	Sequence 1, App11
2	280.4	18.6	2311	1 US-08-103-445-1	Sequence 1, App11
3	182	12.1	1260	1 US-08-385-186-1	Sequence 1, App11
4	181.8	12.0	1245	1 US-08-385-186-14	Sequence 14, App11
5	176.4	11.7	1095	1 US-08-385-186-8	Sequence 8, App11
6	176.4	11.7	1425	1 US-08-385-186-12	Sequence 12, App11
7	172.8	11.5	1978	1 US-08-614-801A-3	Sequence 3, App11
8	172	11.4	1260	1 US-08-385-186-3	Sequence 3, App11
9	167.2	11.1	1827	1 US-08-103-445-3	Sequence 3, App11
10	167.2	11.1	1827	1 US-08-461-690B-3	Sequence 3, App11
11	165.6	11.0	2070	1 US-08-486-342-1	Sequence 1, App11
12	165.6	11.0	2070	1 US-08-473-923-1	Sequence 1, App11
13	165.6	11.0	2070	1 US-08-614-801A-1	Sequence 1, App11
14	165.6	11.0	2076	1 US-08-066-371-1	Sequence 1, App11
15	165.6	11.0	2076	4 US-09-042-494-1	Sequence 1, App11
16	159.6	10.6	2076	5 PCT-US94-05666-1	Sequence 1, App11
17	159.6	10.6	2301	1 US-08-614-801A-5	Sequence 5, App11
18	155.6	10.3	2896	2 US-08-709-923-1	Sequence 1, App11
19	151.2	10.0	1275	2 US-08-614-155B-2	Sequence 2, App11
20	146.6	9.7	1173	2 US-08-614-155B-2	Sequence 2, App11
21	145	9.6	2069	1 US-07-921-178A-1	Sequence 1, App11
22	144.8	9.6	1625	2 US-08-709-923-2	Sequence 2, App11
23	140.4	9.3	1170	2 US-08-501-003A-6	Sequence 6, App11
24	140.4	9.3	1740	2 US-08-501-003A-1	Sequence 1, App11
25	140.4	9.3	1740	5 PCT-US94-01210-1	Sequence 1, App11
26	140.4	9.3	1832	2 US-08-501-003A-2	Sequence 2, App11
27	140.4	9.3	1832	5 PCT-US94-01210-2	Sequence 2, App11

28	139.8	9.3	1173	2 US-08-614-155B-4	Sequence 4, App11
29	139.8	9.3	1173	4 US-09-213-864-1	Sequence 1, App11
30	138.8	9.2	1119	2 US-08-501-003A-7	Sequence 7, App11
31	138.8	9.2	1119	2 US-08-501-003A-8	Sequence 8, App11
32	138.8	9.2	1119	2 US-08-501-003A-9	Sequence 9, App11
33	138.8	9.2	1176	2 US-08-501-003A-10	Sequence 10, App11
34	138.8	9.2	1591	2 US-08-501-003A-5	Sequence 5, App11
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36	138.8	9.2	1671	2 US-08-501-003A-3	Sequence 3, App11
37	138.8	9.2	1671	5 PCT-US94-01210-3	Sequence 3, App11
38	138.8	9.2	1703	2 US-08-501-003A-4	Sequence 4, App11
39	138.8	9.2	1703	5 PCT-US94-01210-4	Sequence 4, App11
40	125.6	8.3	1275	2 US-08-614-155B-4	Sequence 4, App11
41	46.4	3.1	7218	1 US-08-232-463-14	Sequence 14, App11
42	32.8	2.2	5055	4 US-09-242-632A-13	Sequence 13, App11
43	32.6	2.2	1560	1 US-08-194-180-2	Sequence 2, App11
44	32.4	2.1	5994	3 US-09-032-365A-11	Sequence 11, App11
45	31.8	2.1	1273	4 US-09-319-892-3	Sequence 3, App11

ALIGNMENTS

RESULT 1
; Sequence 1, Application US/08461690B
; Patent No. 5670335
; GENERAL INFORMATION:
; APPLICANT: Jan, Lily Y.
; APPLICANT: Jan, Yuh Nung
; APPLICANT: Kudo, Yoshihiro
; APPLICANT: Reuveny, Eitan
; APPLICANT: Slesinger, Paul A.
; TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
; TITLE OF INVENTION: Potassium Channel cDNAs
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,690B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,445
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2310 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 338..1624

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FEATURE:
NAME/KEY: misc_feature
LOCATION: 596..661
OTHER INFORMATION: /note= "Region encoding M1
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 731..781
OTHER INFORMATION: /note= "Region encoding H5
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 806..871
OTHER INFORMATION: /note= "Region encoding M2
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2131..2132
OTHER INFORMATION: /note= "The 'N' occurring at this
OTHER INFORMATION: position represents an 'F'."
US-08-461-690B-1

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Query Match      18.6%; Score 280.4; DB 1: Length 2310;
Best Local Similarity 57.5%; Pred. No. 6.4e-76;
Matches 569; Conservative 1; Mismatches 402; Indels 18; Gaps 3;

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OY 142 agaagacgattcttcacaaagatgcaagctgtaatgtctactcaagacattttga 201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 467 AGGACCCGCTTTGTGAGAAAGATGTGCTATTCATGTTCAGTTATACACGTGGGTG 526
OY 202 gaatgggaagctatgtgtgacatcttcaccactctgtgacacaaagtggcgcat 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 527 AAGGAGACAGAGTACTGCGACAGACATCTTACTACCTGTGCGACATCCGCTGAGAGTGG 586
OY 262 agtttgatatttcttcttactatctctcgtgtgtgtgtgtgtgtgtgtgtgt 321
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 587 ATGCTGGTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
OY 322 tggccatagcttcttcacatctgacatcttcaatgatcagacacacacttgtt 381
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OY 382 gacaaagctcattcttcacagggcccttctgtctccctcagagacccaacacata 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 707 TCGGAGGTCAACAGCTTCAGCGCTGCTCTCTCCATCGAGACCCAGCAACACTT 766
OY 442 gatatgtgtatcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 501
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 767 GCGTATGCTTTCAGGTGTGTGACAGAGAGTGCCTCAATGTGCTGTTCATGGGTATTC 826
OY 502 cagtcacatcttaagttgacataaacttatacttatacttgaagctgagcttgcacaaatg 561
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 827 CAGTCAATGTAGAGCTGCATCATTCAGCGCTTATCATTTGCTCATTCATGGGGAAGT 886
OY 562 gcaactgtcgaagaagagcccaaccattcgttcaagctacttgcacttataagta 621
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 887 GCAAGCCCAAGAGAGAAATGAGACTTGTGCTTCAAGTCACAAATGCTGATGGTGCAT 946
OY 622 agagatgggaagcttgcctcactatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 681
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DB 947 AGGGATGGCAAACTCTGCTTGAAGTGAGAGTGGTAACTTGAAGAGACCACTTGTG 1006
OY 682 gaaggaacagttgagcccaactcgcgtatatacagaagaagcagtgaaaggag--atg 738
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DB 1007 GAAGCTCATGTCCGGGACACAGCTTCTCAATCTAGCATCTTCAGAAAGGGAGATATTC 1066
OY 739 acgatgtcatltaagacactcaatt-----agtcaacgaaccaatcatctctg 766
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DB 1067 CCTTTGGACAGATAGACATCAATGTTGTTGATAGTGAATGTGACCCCATATTTCTA 1126
OY 787 gtcaaccgggttaacttgttcatgaatgtaccatgagagccctctgtatgacctgac 846
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 1127 GTGTCCCATCATCATATGCTTCACGAATAGATGAGACAGCCCTTTATGACTTGTAGT 1186
OY 847 cgaagaagcagtagccaaagataactlttgagatttggtagacttatactacgtgtat 906
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1187 AAGCAGACATTTGACAAATGACAGACTTGAATTTGTTGCTATCTAGGAGCATGTGTCAG 1246
OY 907 tcaactggaacatctcaccaatctagaagctcctatgttcccgaraaatctctcgtgggc 966
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DB 1247 GCGACTGCGATGACACATCAATGACCGGAGTTGTATCTGGCCATGAAATTTCTTGCGGCT 1306
OY 967 catagtttaatgagctcttggaagttaagaagaatlaacaaagtgaactgtctaacg 1026
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DB 1307 CACCGCTATGACCAAGCTGCTCTTTGAGAGAAACACTATATAAGTAGACTATTCAGA 1366
OY 1027 ttgaaggaagtgtggaagta--tatgcccccttctgcagtgtcgaagaactgtgacgtg 1083
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DB 1367 TTCCATTAAGACTTATGAAAGTACTTAACACCCCTTTGTAGTCCAGAGACTTACGACAG 1426
OY 1084 aaagacagcagctccacatagaaaaagca 1113
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DB 1427 AAGAAATACATCTTCAAAATGCAAAATTCA 1456

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RESULT 2
US-08-103-445-1
Sequence 1, Application US/08103445
Patent No. 5492825
GENERAL INFORMATION:
APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yuh Nung
APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan
APPLICANT: Slesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
NUMBER OF INVENTIONS: 26
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco,
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,445
FILING DATE: 06-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 338..1624
FEATURE:
NAME/KEY: misc_feature
LOCATION: 596..661

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OTHER INFORMATION: /note="Region encoding M1
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc.feature
LOCATION: 731..781
OTHER INFORMATION: /note="Region encoding H5
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FEATURE:
NAME/KEY: misc.feature
LOCATION: 806..871
OTHER INFORMATION: /note="Region encoding M2
OTHER INFORMATION: segment."
US-08-103-445-1
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Query Match 18.6% Score 280.4; DB 1; Length 2311;
Best Local Similarity 57.5% Pred. No. 6.4e-76;
Matches 369; Conservative 1; Mismatches 402; Indels 18; Gaps 3;

QY 142 agaagacgaltactacaaagatggcagctgtaactcactcaagcacattttgga 201
DB 467 AGAGGCGGCTTTGAGAAAGATGGTCATTCATGTTTACATTCACACGCGGTGAG 526
QY 202 gaatgggaagcatalgtgtgacatcttccacactctgttgacacccaagtgccat 261
DB 527 AAGGACAGAGTACCTGGCAGACATCTTACTACCTGTGTGCACATCCCGTGAGGTG 586
QY 262 atgttgtatattcttcttcttcttcttcttcttcttcttcttcttcttcttctt 321
DB 587 ATGCTGATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
QY 322 tggcatagacgttctacatggcagatctataatgatccacacacacacttggtt 381
DB 647 TGGTGTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
QY 382 gacacgtcattcttctacagagggccttcttcttcttcttcttcttcttcttct 441
DB 707 TCGAGAGTCAACAGCTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
QY 442 ggaatggtatcgtctgtgttcttgaagaaagtctgtgtgtgtgtgtgtgtgtgt 501
DB 767 GGTATGATGTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 826
QY 502 cagtcacatttaagtgtcatataaatacattatcatttgaagctgcttggccaagt 561
DB 827 CAGTCAATGTAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 886
QY 562 gcaactgtctcgaagagacccaacacttcttcaagctacttgcacttatagatg 621
DB 887 GCAAAACCAAGAAAGAAATGAGACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 946
QY 622 agagatgggaagcttgcctcattggcgcattggtgatttggcgaacacccggtga 681
DB 947 AGGATGAGCAAACTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006
QY 682 gaaggaacagtttagacccaacttctcgtatatacagaagacagttgaaggaag 738
DB 1007 GAAGCTCATGTCTCGGACAGAGCTTCAATATAGATCACTTCAGAAAGAGGAG 1066
QY 739 agcatgtgcatttaagaactcaatt-----agtcaagcaaccaatcatctgt 786
DB 1067 CCTTTGGACAGATTAACATCAATGTTGTTTGTATGATGATGATGATGATGAT 1126
QY 787 gtaccccgtaactcttctcagaatgtgacatgagagcccttgatggccttgac 846
DB 1127 GTGTCCCATCTACTGTCTTCAAGAAATGATGAAGACAGCCCTTATATGACTTG 1186
QY 847 cgcgaagcagtagcgaagaataacttggatgttggtagacatttctatctatctgt 906
DB 1187 AAGCAGGACATTTGACATGAGACTTTGAATGTTGTCTACTGGAAGGACATGAGGAG 1246
QY 907 tccactggacaatctacccaatctagaagctctctatgttcccgaraaatctctgtg 966
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DB 1247 GCGACTGCCATGACAACTCAATCCGAGTTCTGATCTGGCCAAATTAATCTCTG 1306
QY 967 cataggttaatgaltctcttggaaagttaagaggaatatacaagtgaactgtacag 1026
DB 1307 CACCGCTATAGCCAGGCTCTTTGAAAGAAACACTACTACTATAAGTAGACTTCA 1366
QY 1027 tttagaaggaaigtggaagta---tatgcccccttgcagtgccaagcattgagctg 1083
DB 1367 TTCCATAGACTTATGAGTAGACCTTAACACCCCTTTGTGTGTCAGAGACTTAGCAG 1426
QY 1084 aaagaccagcagctccacatagaagaagca 1113
DB 1427 AAGAAATACATCTTCAATGCAATTTCA 1456
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RESULT 3
US-08-385-186-1
; Sequence 1, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Ashford, John P
; APPLICANT: Bond, Chris T
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Steuart Street tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 14210-2-2
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1257
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1260
; OTHER INFORMATION: /note="cDNA encoding human heart
; OTHER INFORMATION: ATP-sensitive potassium channel protein."
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US-08-385-186-1

Query Match 12.1%; Score 182; DB 1; Length 1260;
Best Local Similarity 52.9%; Pred. No. 6.5e-46;
Matches 470; Conservative 1; Mismatches 396; Indels 21; Gaps 3;

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QY 212 gctatgtgttgacatctaccacactctgttgagacccaagtgcgcacatgtgtga 271
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DB 215 ggtacctgagacctcttccacacccctgtgacctgaagcgcccttcaactgtctcg 274
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QY 272 tatttcttatactatctctctgtgtgtatatttgccctgtcttggctcatg 331
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DB 275 tcttcacacatggtttacactgttcacctgctgtcttcgcttcaattggctcattgg 334
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QY 332 cctttcatcatgtgcgtctattaaat-----gattccacacatcacactgtttgaca 385
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DB 335 cttaataatccgggggtgacctgacacatgttgccgaccacacacatgattccttggtaaa 394
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QY 386 acgtccatctcttccacaaaggcccttctgtctccctagaagccaacacacataagat 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 395 acctcagatggttcggttcggtccgttccgttccatctgacacacacacacacattgggt 454
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DB 575 accccaaagaaagagagggagacccctcatgttttccaaacagacgacatctccatcgagg 634
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QY 1031 aagggaagtgtgaagatataagccccccttgcagtgccaagaacatgtg 1078
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DB 1055 atgatatcctatgagacacacacacacacacacacacacacacacacacacacacac 1102
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US-08-385-186-14
; Sequence 14, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:

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APPLICANT: Adelman, John P
APPLICANT: Ashford, Michael J
APPLICANT: Bond, Chris T
TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,186
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ. ID NO. 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 22..1242
OTHER INFORMATION: /note= "Encodes a full-length or
OTHER INFORMATION: nearly full-length human pancreatic beta cell
OTHER INFORMATION: ATP-sensitive potassium channel protein: Seq ID.
US-08-385-186-14
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Query Match 12.0%; Score 181.8; DB 1; Length 1245;
Best Local Similarity 52.7%; Pred. No. 7.5e-46;
Matches 474; Conservative 1; Mismatches 403; Indels 21; Gaps 3;

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QY 272 tatttcttatactatctctctgtgtgaltgaltgtgtctgtcttggctcatg 331
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DB 257 tttttgtcatgttttgcacagtgacctgcttcttttggaaatgactgtgtgtgatcg 316
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QY 332 cctttcatcatgtgcgtatcat-----taaatgacacacacacacacacttgtgtgaca 385
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QY 386 acgtccatcttccacaaaggcccttctgtctccctagagacccaacacacacataagat 445
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DB 377 acctcaacgggttcgtctctgttcttttttttttttttttttttttttttttttttttttttt 436
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QY 446 atggtatcgcgtgctgtaactgaagaatgtctctgagccgtgcatatggtatcccaat 505
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Db 437 ATGGCTACCGGGGTCATACAGATAAATGCCGGAGGAATATTTCTCTTATATCAAT 456
QY 506 ccaatcttaagtgtcatcataataacttataccttatacaltgagagctgcccgaatgagca 555
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Db 497 CTGTGTTGGGGTCATGTCAATGCATTCATGCTGGATGCATGTGTGTAATAATCTCTC 556
QY 566 ctgctgagagagagagcccaacatcgtcttgcgtacttgcactatagatagag 625
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 AACCCAGAGAGAGAGGAGAGACCTGTCTTTTCCACCAATGAGATGATCTCCATGGGG 616
QY 626 atggaagcttctgctcatatggtgcagatggtgatttgcggccaacacagtgtagaag 685
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Db 617 ATGGGAACCTGTGCTGATGTCTCCGGGTAGGGACCTTAGGAATGCCCATTTGTGGAGG 676
QY 686 gaacagttgagagcccaactctccgctatacagaagaagcagtgaggagag---atgacga 742
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 677 CTTCATCAAGAGCCAAAGTTGATCAAAATCCAAACAGACCTGGAGGGGAGCTTCATCCGT 736
QY 743 tggcatttaagagcccaaatla-----gtcaagagcccaatcatctgtgca 790
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 737 TGAACCAAGAGAGATATCAAGTGAAGGATTAACAGGGGGATGACCGTCTTCTGTGT 796
QY 791 ccccggtlaactatgtccatgaatgaacatgagagccctctglatgcccctgacgca 850
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Db 797 CACCGCTGATCATTCAGCAATGAATTAACCAACAGAGTCTTCTGGAGATCTCCAAAG 856
QY 851 aagcagtagcgaagaataacttggagatttggtagaattatctatactgtagatcca 910
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Db 857 CCCAGCTGCCAAAGAGAGAACTGGAATGTGTGTCATCTAGAAAGAAATGCTGGAAGCCA 916
QY 911 ctggaacatctcaacaaatctagaagctctatgcttcccgaraattctctgagccata 970
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QY 1031 aaggaaagtgtggaagtatatgcccccttctgacgtgcgaagcaatgagctgtaaaagac 1089
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APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1095
OTHER INFORMATION: /note="Sequence of cDNA clone
Patent No. 5744594
OTHER INFORMATION: encoding a portion of rat pancreatic beta-cell
OTHER INFORMATION: ATP-sensitive potassium channel protein."
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1092
US-08-385-186-8

Query Match 11.7%; Score 176.4; DB 1; Length 1095;
Best Local Similarity 51.8%; Pred. No. 3.2e-44;
Matches 461; Conserved 1; Mismatches 407; Indels 21; Gaps 2;

QY 212 gctatggttgatgacatcttccacacactctgtgagacccaagtggtgcatatgtgtga 271
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QY 272 tatctcttatactatattctctggttgatgtatgtgctctgttcttgcatag 331
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QY 332 ccttcaatcagtcgactat-----taaatgatacagacatacaacttgtgtgaca 385
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Db 227 ACCTCAACGGGTTGTCTCCGCTTTTATCTCATATAGACAGAAACACCATTTGGTT 286
QY 446 atggtatcgcgtgctgtaactgaagaatgtctctgagccgtgctcatatggtatcccaat 505
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QY 506 ccaatcttaagtgtcatcataataacttataccttatacaltgagagctgcccgaatgagca 565
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Db 347 CCGTGTGGGGTCATATGTCACAGCGCTTCATGATGTAGATGTATGTTTGAATAATATCCC 406
QY 566 ctgctgagagagagcccaacacatcgttcaagctacttgcacttataagtagagag 625
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Qy 626 atggaagcttgcctcatgtgycgcatgtgtatlttcggccaacacagtgtagaag 685
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Db 527 CCTCCATGACGACCAAGTTGATCAAGTCCAAAGACACTTCAGAGGGGAGATTCATCCCC 586
Qy 738 -----gacgatggcatttaagaacccaattagtcacagcaaatcctcgtgca 790
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 647 CACGGCTGATTATTAGCCATGAATTAACCAAGAGATGCCCTTGCGAGATCTTCCAAG 706
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Db 707 CCCAGCTGCTTAAAGAGAGACTGGAGATTGTGTCATCTCGAGGGAATGTGGAAAGCA 766
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Db 827 GGTTCACACACGATCCTGACACTGGAGAGACGGGTCTCTATGAGTTGATCAACACACTTCC 886
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RESULT 6

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US-08-385-186-12
: Sequence 12, Application US/08385186
: Patent No. 5744594
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: GENERAL INFORMATION:
: APPLICANT: Adelman, John P
: APPLICANT: Ashford, Michael J
: APPLICANT: Bond, Chris T
: TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
: TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: Stewart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/385,186
: FILING DATE: 07-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/288,510
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/193,372
: FILING DATE: 08-FEB-1994
: ATORNEY/AGENT INFORMATION:
: NAME: Kruse, No. 5744594man J.
: REGISTRATION NUMBER: 35,235
: REFERENCE/DOCKET NUMBER: 14210-2-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043

```

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: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1425 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 56..1330
: NAME/KEY: misc feature
: LOCATION: 1..1425
: OTHER INFORMATION: /note="Encodes rat pancreatic beta
: OTHER INFORMATION: cell ATP-sensitive potassium channel protein."
US-08-385-186-12

Query Match 11.7%; Score 176.4; DB 1; Length 1425;
Best Local Similarity 51.8%; Pred. No. 3.6e-44;
Matches 461; Conservative 1; Mismatches 407; Indels 21; Gaps 2;

Qy 212 gctatgtgtgacatcttcaacactctgtggaacaccagtgagccatagtgttga 271
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Db 285 CATACCTACGACGACATCTTCAACACCCCTGGTGACCTAAAGTGAAGATTCACCTATTGA 344
Qy 272 tatttcttatactatctctcgtggtgattgataatttgctctgcttcttgctcagtag 331
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Qy 446 abgttatcgtctgtgtactgaagaagttcgtgagccgtgctcagtgtagtcctcagc 505
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Qy 506 ccatttaagtgtcatataataatcattatcatattgagagcgtccttgccaaatagtgaa 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 566 ctgctgaagaagagcccaacacatctgcttcaagtaacttgcacttaagtagtagagag 625
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Db 705 ATGGGAACATGCTGCTGATGTTCCGGGATGGGAGTGAAGAAATTCACATAGTGAGG 764
Qy 686 gaacagttagagcccaacttccgcctacataagaagaagaaaggaagat----- 737
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Db 765 CCTCCATGACGACCAAGTTGATCAAGTCCAAAGACACTTCAGAGGGGAGATTCATCCCC 824
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Db 825 TCACACAGACGAGATATCAAGTACAGGCTACTACACCGGGGATGACCGACTCTTTCTCGTGT 884
Qy 791 ccccgtaactatgtccatgaatltgaccatgagagccctctglatgcccctgacgca 850
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Qy 851 aagcagtgcccaagataactttgagatttggtagacattatcctacatctgtgtatcca 910
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Qy 911 ctggaacatcccaactcagaagctcctatgttcccgaraaatctctcgtgagcata 970
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Db 1005 CAGGAATGACGTGCCAAGCTCGAAGCTCTACGTACACAGTAGATCTGTGGGTTTACC 1064

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,186
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1260
OTHER INFORMATION: /note="cDNA for rat heart
FEATURE:
NAME/KEY: ATP-sensitive potassium channel protein."
LOCATION: 1..1257
FEATURE:
NAME/KEY: primer_bind
LOCATION: 472..491
OTHER INFORMATION: /note="Sequence corresponding to
Patent No. 5744594
OTHER INFORMATION: Seq. I.D. No. 5744594 5."
FEATURE:
NAME/KEY: primer_bind
LOCATION: 632..651
OTHER INFORMATION: /note="Sequence complementary to
Patent No. 5744594
OTHER INFORMATION: Seq. I.D. No. 5744594.6"
US-08-385-186-3
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Query Match 11.4% Score 172; DB 1; Length 1260;

Best Local Similarity 51.2% Pred. No. 7.6e-43; Matches 465; Conservative 1; Mismatches 421; Indels 21; Gaps 2;

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QY 192 catttttgagagatggaggaagctatggttgacacatcttcacacactctgttgagaccaa 251
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Db 195 CAATGTACAGGAACCTACGCTTAAGTACCTTACACACCTGCTGAGACTCA 254
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QY 232 gtggcgacatattgttgatattcttctatctatattctctcgttgatattgg 311
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QY 366 catcacacttggttgacaacgctcatcttccacagagccttcttgctccctaga 425
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RESULT 9
US-08-103-445-3
Sequence 3, Application US/08103445
Patent No. 5492825

GENERAL INFORMATION:

APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yuh Nung

APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan

APPLICANT: Slesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier

TITLE OF INVENTION: Potassium Channel cDNAs
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert

STREET: 4 Embarradero Center, Suite 3400
CITY: San Francisco,

STATE: California
COUNTRY: USA

ZIP: 94111-4187
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,445
FILING DATE: 06-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1889
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1827 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 59..1564
FEATURE:
NAME/KEY: misc_feature
LOCATION: 314..379
OTHER INFORMATION: /note= "Region encoding MI
OTHER INFORMATION: segment."
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NAME/KEY: misc_feature
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LOCATION: 530..595
OTHER INFORMATION: /note= "Region encoding M2
OTHER INFORMATION: segment."
US-08-103-445-3

Query Match      11.1% Score 167.2; DB 1; Length 1827;
Best Local Similarity 50.9%; Pred. No. 2,7e-41;
Matches 486; Conservative 1; Mismatches 444; Indels 23; Gaps 3;

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QY 208 ggaagctatgtgtgtgacatcttaccacctctgtgacaccaaagtggcgccatagtgt 267
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DB 491 GCGTATGGCTACCGCTACATACCGAAGTGGCCCGAGGCGCATCATCTTCTTCTTTC 550
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QY 562 gcaactgtcgaagaagagcccaaacatcttcgtttcagctacttgcacttataatgata 621
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DB 611 TCCAGGCCCAAAAGAGCGCGAGACCTCATGTTTACGAGCATCGCGCTATTTCCATG 670
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QY 622 agaatgtggaagcttgcctcatgtgacgtatgtgtatgttctggccaaccacgtgta 681
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QY 682 gaagaaagatgaagcccaacttctccgcatatcagaagaacagtgaaaggaatgacg 741
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DB 731 TCCGCGAGATCCCTGCATGCTCTCAAAATCT-CGCGAGACCTCGAGGATGATTTCT 789
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QY 742 atggcat-----ttaagacctcaaatatgaatgaacgaaccaatcatcct 785
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DB 790 ACCCTTGACCACTTGACATGATGATGTTTATGATACAGGCGAGATCAACTTTTCT 849
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QY 786 ggtacccccgttaactatgtccatgaataatgacatgagagccctctgttccttga 845
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DB 850 TGTGCCCCCTCACCATTTCACAGTGTGATGCCAAAGCCCTTTTATGACCTATC 909
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 846 ccgcaagcagtagcacaagaatcttgagatttggtagcatlactatctactgtgtga 905
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DB 910 CCACGGAAGCATGCAAACTGAACAGTTGAGTGTGCTCATCTCGAAGGCAATCGTGA 969
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 906 ttccactggaacatcttcaacatctagaagcttccatgttcccgataraattctctgag 965
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 970 AACCAAGAGGATGACTTGTCAAGCTCGAACATCATACCAAGATGAAGTTCTTTGGGG 1029
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 966 ccataggttaatgtagtcttgaagatgaaggaagattatacaagtgaactgtcttaca 1025
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DB 1030 TCATGCTTTTTCCTCTGAATTTCTTTAGAAAGAGATTTTAAAGTCGATTAATCTCCA 1089
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QY 1026 gttgaagaagatgtggaagatatatgcccccttctgacgtgccaaagcatgtga 1079
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DB 1090 GTTCATGCAACCTTGAAGTCCACCCCTCCGTACAGTGTGAAGAGCAGAGA 1143
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```
RESULT 10
US-08-461-690B-3
Sequence 3, Application US/08461690B
Patent No. 5670335
GENERAL INFORMATION:
APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yuh Nung
APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan
APPLICANT: Slesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,690B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,445
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619-1/MHD/JPB
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1827 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 59..1561
FEATURE:
NAME/KEY: misc.feature
LOCATION: 314..379
OTHER INFORMATION: /note="region encoding M1
OTHER INFORMATION: segment.
FEATURE:
NAME/KEY: misc.feature
LOCATION: 455..505
OTHER INFORMATION: /note="region encoding H5
OTHER INFORMATION: segment.
FEATURE:
NAME/KEY: misc.feature
LOCATION: 530..595
US-08-461-690B-3

Query Match 11.1%; Score 167.2; DB 1; Length 1827;
Best Local Similarity 50.9%; Pred. No. 2.7e-41;
Matches 486; Conservative 1; Mismatches 444; Indels 23; Gaps 3;

148 ccatcttccaaagaatgcaagctgtaatgtctacttcaagaacattttgagaatg 207
191 CGGTTGTGACAGAAACGCTGCTGCAATGTCAGACGCAACCTGGGACAGAGACC 250
208 ggaagctatgtgtgacacatctaccactctgtggaacaaagtggcgcatatgtt 267
251 AGTCGCTACCTTCCGACCTCTTCACTACCTGCTGATCTCAAGTGGCGCTGAACTTC 310
268 gggatatttcttactatattctctcgtgtgtgatatttggctctgtcttggctc 327
311 TTTATCTTCAATCTCACTACCTGCTGCTTCAATGCGCTGCAATGCTGCTGCTG 370
328 atagcttccatcatggcgatcatttaaatgacacag-----acataacacttgg 381
371 ATGGCTTATACCGGGGCGACCTGGAACAAAGCCCATGTCGCAACTACATCCCTGTG 430
382 gacaagctcattcttccacaaaggcccttggctcctccctagagacccaaccacata 441
431 GCCAATGTCTATTAATCTCCCTCTGCTTCTTCTTCAATCGACCGAGCCGACCATC 490
442 ggtataggtatgctgtgttactgaagaatgttctgtggcggtgcacatggtatc 501
491 GGCTATGGCTACGCTACACACCGAAGTGGCCCGAGGGGCATTCCTTTCTTTTC 550
502 cagtcacttcaatgcaatcaataacttatacttgaagctgtgctggccaatg 561
551 CAGTCCATCTTGGCTCCATGCGAGCGCTTCTCTCATCGGCTGCATGTTCAATCAATG 610
562 gcaactgtcgaagaagagcccaaacattcgtttcagctacttctgcaactatagtgat 621
611 TCCAGCGCCAAAAGCGCGGAGACCTCATGTTTAGCAGCATGGGTTATTTCCATG 670
622 agagatgggaagcttggctcctcattgtggcgcatgtgtatatttggccaacaacggtgta 681
671 AGGAGACGAAACCTCACTCATGTTCCGGGTGGGCAACCTGCCCAACACCAACATGTC 736
682 gaaggaacagttgagagcccaactctcgcctatacagaagacagtgaggaagagag 741
731 TCCGCGCAGATCCGCTGCAAGCTGCTCAAAATCT-CGGCAGACACCTGAGGGTGTTC 789

QY 742 atggcat-----ttaagacctcaattagtcacagaccacatcct 785
DB 790 ACCCCTTGACCACTTGAACGTGATGATTTAGTACAGGGGCGAGATCAACTTTTCT 849
QY 786 ggtcaccgcggaactatgtccatgaatgtgacaatgagagccctctgtatgccttga 845
DB 850 TGTGTCCTCTCACCATTGTGCGACGTGATGTATGCAAAACCCCTTTATGACCTATC 909
QY 846 ccgcaagaagtagccaagaataactttagaatttggtagcatttatctatctgtgta 905
DB 910 CCAGGACAGCATGCAAACTGAAACAGTTGAGGTGCTCATCTCTGAAGCGCATCGTGA 969
QY 906 tccactggaacatctcaccatctagaagctcctatgttcccgaraaattctcggg 965
DB 970 AACACAGGAGATGACTGTCAAGCTGCAACATCATACCCAGAGATGAACTTTGGGG 1029
QY 966 ccataggttaatgagtcttggaaagttaaggaagtagtatacgaagtgaactgtctaa 1025
DB 1030 TCATCGTTTTCCTGATTTCTTTAGAGAGAGATTTCTTAAGTGATTAATCTCCCA 1089
QY 1026 gtttgaagaagtgtagaagtagatagcccttggcagtgccgaagcaattgga 1079
DB 1090 GTTCATGCAACCTTGAAGTCCCAACCCCTCGTACAGTGTGAAGAGACAGGA 1143

RESULT 11
US-08-486-342-1
Sequence 1, Application US/08486342
Patent No. 5728535
GENERAL INFORMATION:
APPLICANT: Lester, Henry A.
APPLICANT: Dascal, Nathan
APPLICANT: Lim, Nancy F.
APPLICANT: Schreimayer, Wolfgang
APPLICANT: Davidson, No. 5728535man
TITLE OF INVENTION: DNA Encoding Inward Rectifier,
TITLE OF INVENTION: G-Protein
TITLE OF INVENTION: Activated, Mammalian, Potassium KGA Channel and
TITLE OF INVENTION: Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,342
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Treacart, Richard F.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-62319/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs


```

: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 32..1534
: US-08-486-342-1

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```

Query Match      11.0%; Score 165.6; DB 1; Length 2070;
Best Local Similarity 50.8%; Pred. No. 9e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

```

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OY 148 cgattacttcaaaagtgtgagctgtatgtctacttcaagccatttttgagaag 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 CGGTTCTGGACAGAAAGCGTGGTGAATGCAAGCAGGCAACCTGGGAGAGACC 223
OY 208 ggaagctatgtgtgtacatcttcaaccctctgtgagacaaagtgcgcatagtt 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 AGTGTCTACCTTTCCGACCTCTTCACTAACCTGGTGATCTCAAGTGGCGTTGGAACCTC 283
OY 268 gtgataattcttattattattctctgtgtgtatgtatgtgtctgtcttggctc 327
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Db 284 TTTATCTTCATCTCCACCTACACCGTGGCTGTCTCATGCGCTCATGTGGTGGGTG 343
OY 328 atagccttcaatcatgcatctataatgatccag-----acatcacacctgtgt 381
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OY 382 gacaagctcattcttctacagagggccttctgtctccctagagaccacacata 441
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Db 404 GCCAATGTCTATACCTTCCCTCTGCTCTCTTCTTCATCGAGACGAGCCACCATC 463
OY 442 ggaatgttatgcgtgtgttactggaagatgtctgtgcggtgtcatgtgtatctct 501
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Db 464 GGGCTATGGCTACCCCTCATCACCGCAAGTGGCCGAGGCGCATCATCTTTCTTTTC 523
OY 502 cagtcacatctaagttcatcataataacacctatcatcttgtagtgctgtggccaatg 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CAGTCCATCTTGGCTCATCTGTGAGCGCTTCTCTCATCGGCTGCATGTTATGAAGTGTG 583
OY 562 gcaactgtcgaagagagcccaaacatttgccttgctacacttctactatagatg 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TCCAGGCCCAAAAGGCGCGGAGACCCCTCATGTTAGCGAGCATGGGGTTATTTCATG 643
OY 622 agagatgtggaagcttgcctcatgtgtgcgcatgtgtgattcttgccaaacagtgta 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 AGGAGCGGAAACTCACCTCTCATGTTCGGGTGGGCAACCTGCGCAACAGCCACATGCTC 703
OY 682 gaagaaacagttagagcccaacttctcgcctatataagaagacagttgaagagatgacg 741
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Db 704 TCCGCGAGATCCGCTGCAAGCTCTCAAACT- CGGCAAGACCTGAGGGTGAAGTTCT 762
OY 742 atggcat-----ttaagaacctcaaatltagtcaacgaacaaatcatctc 785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 ACCCTTGACCAACTTGACATGATGATGATGTTTATTAGACAGGGGACATCAACTTTTCT 822
OY 786 gyltaccctggtaactatgttccatgtgaattgacatgagagccctctgtatgccttga 845
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Db 823 TGTGTCCCTCTCAACCTTTGGCCAGCTGATGATGCCAAAAGCCCTTTTATGACCTATG 882
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Db 883 CCAAGCAAGCATGCAAACTGATGAGTTGAGAGTGTGTCTCTCTGGAAGGACATCGTGA 942
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Db 943 AACCAACAGGATGACTGTCAAGCTCGAATCATACACCAAGATGAAGTTTCTTTGGGG 1002
OY 966 ccctaggtttaaagtgtctgtgagagttgaagagattatcaagaatgtaactcttaca 1025
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Db 1003 TCATCGTTTTCCTCCGTGAATTTCTTTAGAAAGATGCTTTTAAAGTCGATCTACCCCA 1062

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OY 1026 gtttgaagaaagtgtggaagatatagtccctcttgcagtgccaagcaattgga 1079
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Db 1063 GTTCATGCAACCTTTGAAGTCCCAACCCCTTCCTGATAGTGTGAAGAGCAGGA 1116

```

```

RESULT 12
US-08-473-092-1
: Sequence 1, Application US/08473092
: Patent No. 5734021
: GENERAL INFORMATION:
: APPLICANT: Lester, Henry A.
: APPLICANT: Dascal, Nathan
: APPLICANT: Lim, Nancy F.
: APPLICANT: Schreimayer, Wolfgang
: APPLICANT: Davidson, No. 5734021man
: TITLE OF INVENTION: DNA Encoding Inward Rectifier,
: TITLE OF INVENTION: G-Protein Activated, Mammalian,
: TITLE OF INVENTION: Potassium KGA Channel and Uses
: NUMBER OF SEQUENCES: 2

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Flehr, Hohbach, Teal, Albritton
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,092
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-62317/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

```

```

INFORMATION FOR SRO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```

```

FEATURE:
NAME/KEY: CDS
LOCATION: 32..1534
US-08-473-092-1

```

```

Query Match      11.0%; Score 165.6; DB 1; Length 2070;
Best Local Similarity 50.8%; Pred. No. 9e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

```

```

OY 148 cgattacttcaaaagtgtgagctgtatgtctacttcaagccatttttgagaag 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 CGGTTCTGGACAGAAAGCGTGGTGAATGCAAGCAGGCAACCTGGGAGAGACC 223
OY 208 ggaagctatgtgtgtacatcttcaaccctctgtgagacaaagtgcgcatagtt 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 AGTGTCTACCTTTCCGACCTCTTCACTAACCTGGTGATCTCAAGTGGCGTTGGAACCTC 283

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OY 268 gtgataatttcttatacttatactctcgtggtgataattggtctcttcttggctc 327
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OY 328 atagccttcatcatggtgcatcattaaatgacag-----acatacaaccttgtt 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY 382 gacaacgtccatcttcccaaggcccttcttctccctagaagcccaaacacata 441
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OY 442 ggaatggtatcgtcgtgttactgaagaatgtctgtggtcggtgcatggtatcctc 501
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OY 502 cagtcatacttaagtgtcatcaataaactctatactatgttgagctgcttggcacaatg 561
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Db 524 CAGTCCATCTCTGGCTCCTGTCATGTCGAGCGCTTCTCTCATCGGTCATGTCATCAAGATG 583
OY 562 gcaacgtcgaagaagagcccaacacatcgttcaagctacttgcacttaagtatg 621
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 584 TCCACACCCCAAAAAGCGCGCGAGACCCCTATGTTTAGCGAGCATGGCTTATTTCATG 643
OY 622 agagatgggaagccttgcctcatgtggtgcatgtgtatttgcgcacaacacagtgta 681
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Db 644 AGGAGCGGAAACACTACTCATGTCCGGGTGGGAGCACTGGCAACACCATGATGTC 703
OY 682 gaaggaacagltgagcccaacttccgctatacagaagacagltgaaggaagtgaag 741
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 704 TCCGCGCAGATCGCTGCAAGCTGCTCAATCT-CCGCGACAGACCTGAGGGTGTCT 762
OY 742 atggcat-----ttaagaacctcaattgtcaagcccaatcactcct 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 763 ACCCCTTGACCACTTGACTGATGTAGTTTATGACAGGGGACAGATCACTTTTCT 822
OY 786 ggtacccccgttaactattgtcgaatattgacatgagagccctctgtatgcccc 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 823 TGTGTCCCTCTCACATTTGACAGCGTATGTCGCAAAAGCCCTTTATGACCTATG 882
OY 846 ccgcaagacagtgcccaagaataacttggatgttgggtgacatttactactgtgta 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 883 CCAGCGAAGCATCAAACTGAAACAGTTCGAGTGTCTCATCTCGAAGGCAATCGTGA 942
OY 906 ttccactgtgacatctccacatctagaagctctatgttccccgagaaatctctgag 965
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OY 966 ccaatggttaatgattgtcttggaaagltgaaggaagltatcaagaatgaaatgtctaca 1025
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Db 1003 TCATCGTTTTTCCCTGTAATTTCTTTAGAAAGATGCTTTAAAGTCAATTAACCCA 1062
OY 1026 gtttgaagaaggtggaagatatatgcccccttggcagtgccaagaattgga 1079
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1063 GTTCCATGACACTTGAAGTCCCAACCCCTCCGTACAGTGAAGAGAGAGGA 1116

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RESULT 13

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US-08-614-801A-1
: Sequence 1, Application US/08614801A
: Patent No. 5744324
: GENERAL INFORMATION:
: APPLICANT: Lester, Henry A.
: APPLICANT: Davidson, No. 5744324man
: APPLICANT: Kofuji, Paulo
: TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
: TITLE OF INVENTION: MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco

```

```

: STATE: California
: COUNTRY: United States
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/614,801A
: FILING DATE: 07-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/066,371
: FILING DATE: 21-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Treacartin, Richard F.
: REGISTRATION NUMBER: 31,801
: REFERENCE/DOCKET NUMBER: A-63098/RFT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299
: INFORMATION FOR SEQ. ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2070 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 32..1534
: US-08-614-801A-1

```

```

Query Match 11.0%; Score 165.6; DB 1; Length 2070;
Best Local Similarity 50.8%; Pred. No. 9e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

```

```

OY 148 cgaattcctcaagaagltgacgtcgttaatgtctacttcaagacacatttttggagaatg 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 164 CGGTTCTGGACAAAGAGGTGCTGTCATATGTCAGACGCGCAACTGGCGACGAGACC 223
OY 208 ggaagctatgtgttgaacatcttcacacactctgttgacacaaagltgcgcatagttt 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 224 AGTCGACTCTTCCGACCTCTTCACTACCTGCTGATCTCAAGTGGCGTGAACCTC 283
OY 268 gtgataatttcttactatattctctcgtgtgtgattgatatgtgtcgtcttggctc 327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 284 TTTATCTTCATCTCCTACCTACCTACCGTGGCTGCTCTTCATGCGCTCATGTGTGGTG 343
OY 328 atagccttcatcatggtgagatcttataatgatccag-----acatacaaccttgtt 381
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RESULT 15

US-09-042-494-1

Sequence 1, Application US/09042494

Patent No. 6255459

GENERAL INFORMATION:

APPLICANT: Lester, Henry A.

APPLICANT: Dascal, Nathan

APPLICANT: Lim, Nancy

APPLICANT: Schreimbayer, Wolfgang

APPLICANT: Davidson, No. 6255459man

TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN

TITLE OF INVENTION: ACTIVATED, MAMMALIAN POTASSIUM KGA

TITLE OF INVENTION: CHANNEL AND USES THEREOF

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,494

CLASSIFICATION:

FILING DATE: 16-MAR-1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/066,371

FILING DATE: 21-MAR-1993

ATTORNEY/AGENT INFORMATION:

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REFERENCE/DOCKET NUMBER: A-59891-1/RFT/DAV

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2076 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 32..1534

US-09-042-494-1

Query Match

Best Local Similarity 11.0%; Score 165.6; DB 4; Length 2076;

Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

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DB 164 CGGTTGCGTGAAGAACGTCGTCATGTGCAACGACGACGTCGAGCGAGACC 223

QY 208 ggaagctatggttgactcttcaactcttggagacacaaagtggcgcatagttt 267

DB 224 AGTCGCTACCTTCGACCTGTCCTCACTACCTGTCGATCTCAAGTGGCTTGAACCTC 283

QY 268 gtgataattcttattctatctctcgtgtgataattggcctcgtcttggcgc 327

DB 284 TTATCTTATCTCTACCTACACGCGGCTGCTTTCATGCGCTTCATGCTGCTG 343

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Search completed: October 5, 2002, 04:00:43
Job time: 4663 sec

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